EXPRESSION VECTORS

This application claims priority to provisional appl. 60/215,851, filed 3 July 2000.

FIELD OF THE INVENTION

The present invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell.

BACKGROUND OF THE INVENTION

Methods for expression of recombinant proteins in bacterial host are widespread and offer ease of use and purification of the recombinant product. However, use of these systems for the expression of eukaryotic proteins is often limited by problems of insolubility and lack of proper post-transcription and post-translational processing (*see, e.g.*, U.S. Pat. No. 5,721,121, incorporated herein by reference). Thus, eukaryotic expression systems are generally used for the expression of eukaryotic proteins. In particular, the pharmaceutical biotechnology industry relies heavily on the production of recombinant proteins in mammalian cells. These recombinantly produced proteins are essential to the therapeutic treatment of many diseases and conditions. In many cases, the market for these proteins exceeds a billion dollars a year. Examples of proteins produced recombinantly in mammalian cells include erythropoietin, factor VIII, factor IX, and insulin. In addition, recombinant antibodies are often used as therapeutic agents. Clinical applications of recombinantly produced proteins, in particular antibodies, often require large amounts of highly purified proteins. Proteins are generally produced in either mammalian cell culture or in transgenic animals.

Vectors for transferring the gene of interest into mammalian cells are widely available, including plasmids, retroviral vectors, and adenoviral vectors. Retroviral vectors are widely used as vehicles for delivery of genes into mammalian cells (*See e.g.*, Vile and Russell, British Medical Bulletin, 51:12 [1995]). However, current methods for creating mammalian cell lines for expression of recombinant proteins suffer from several drawbacks. (*See, e.g.*, Mielke *et al.*, Biochem. 35:2239-52 [1996]). Episomal systems allow for high expression levels of the recombinant protein, but are frequently only stable for a short time period (*See, e.g.*, Klehr and Bode, Mol. Genet. (Life Sci. Adv.) 7:47-52 [1988]). Mammalian cell lines

containing integrated exogenous genes are somewhat more stable, but there is increasing evidence that stability depends on the presence of only a few copies or even a single copy of the exogenous gene. Vectors are often unstable, resulting in a decrease in the level of protein expression over time.

Based on overall product yield, expression of recombinant proteins in animals results in higher yields, relative to expression in cell culture (*See e.g.*, Werner *et al.*, Arzneimittelforshcung, 48:870 [1998]; Pollock *et al.*, J. Immunol. Methods, 231:147 [1999]). However, expression in transgenic animals is limited by methods of producing transgenic mammals, variation in production and purity, and the life span of the animal.

Thus, despite continued efforts in the field, vectors for high level, continuous expression of one or more proteins in a host cell remain needed in the art.

SUMMARY OF THE INVENTION

The present invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell.

In some embodiments, the present invention provides a hybrid α-lactalbumin promoter comprising at least one portion derived from a first mammalian α-lactalbumin promoter and at least one portion derived from a second mammalian α-lactalbumin promoter. The present invention is not limited to portions derived from any particular α-lactalbumin promoter. Indeed, portions from a variety of α-lactalbumin promoters are contemplated, including, but not limited to bovine, human, ovine, caprine, and murine α-lactalbumin promoters. In other embodiments, the present invention provides a nucleic acid comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1 and sequences hybridizable to SEQ ID NO:1 under low stringency conditions, wherein the nucleic acid contains sequences derived from at least two mammalian sources and causes mammary specific gene expression. In still other embodiments, the present invention provides a nucleic acid sequence encoding a hybrid bovine/human alpha lactalbumin (αLA) promoter/enhancer (*i.e.*, SEQ ID NO:1) and sequences that are hybridizable to a hybrid bovine/human α-LA promoter under low to high stringency conditions. In preferred embodiments, these sequences drive the expression of an exogenous gene in the mammary gland of a transgenic animal. In some embodiments, the

hybridizable sequence comprises human and bovine elements. In other embodiments, the present invention provides a vector containing the nucleic acid sequence of hybrid bovine/human α-LA promoter. In some embodiments, the vector is a retroviral vector. In still further embodiments, the present invention provides a host cell containing a vector containing a hybrid bovine/human α-LA promoter.

The present invention also provides a nucleic acid encoding a mutant RNA export element (PPE element; SEQ ID NO:2) and sequences that are hybridizable to a mutant PPE element. In some embodiments, the sequences hybridizable to a mutant PPE element contain ATG sequences that have been mutated at at least one of the positions corresponding to nucleic acid residues 4, 112, 131, and 238 of the wild-type PPE element. In preferred embodiments, these sequences enhance the export from the nucleus of the RNA to which they are operably linked. In other embodiments, the present invention provides a vector containing the nucleic acid sequence of the mutant PPE element. In some embodiments, the vector is a retroviral vector. In still further embodiments, the present invention provides a host cell containing a vector that contains a mutant PPE element.

The present invention also provides a nucleic acid encoding an IRES coding sequence and a signal peptide coding sequence, wherein said IRES and signal peptide coding sequences are adjacent to one another. In some embodiments, the IRES/signal peptide sequence comprises SEQ ID NO:3 or SEQ ID NO:12 and sequences that are hybridizable to these sequences under low stringency conditions. In preferred embodiments, these sequences interact with a ribosome and provide for the secretion of proteins to which they are operably linked. The present invention is not limited to any particular signal sequence peptide. Indeed, it is contemplated that a variety of signal peptides find use in the present invention. In some embodiments, the signal peptide sequence is selected from alpha-casein, human growth hormone, or α-lactalbumin signal peptide sequences. In other embodiments, the present invention provides a vector containing the nucleic acid sequence of the IRES/signal peptide sequence. In some embodiments, the vector is a retroviral vector. In still further embodiments, the present invention provides a host cell containing a vector that contains a IRES/signal peptide sequence.

The present invention also provides methods for producing a protein of interest. In

some embodiments, the methods comprise providing a host cell and a vector containing at least one exogenous gene operably linked to a bovine/human hybrid α-lactalbumin promoter and introducing the vector to the host cell under conditions such that expression of the protein encoded by the exogenous gene is expressed. In some embodiments, the vector further contains a mutant RNA export element. In other embodiments, the vector contains at least two exogenous genes. In still further embodiments, the two or more exogenous genes are arranged in a polycistronic sequence separated by an internal ribosome entry site/bovine α-lactalbumin signal peptide.

The present invention also provides methods for expressing at least two proteins in a polycistronic sequence. In some embodiments, the proteins are unrelated, while in other embodiments, the proteins are subunits of a multisubunit protein. In some preferred embodiments, the present invention provides methods for producing an immunoglobulin including providing a host cell and a vector comprising a first exogenous gene and a second exogenous gene, wherein the first exogenous gene encodes a first immunoglobulin chain and wherein the second exogenous gene encodes a second immunoglobulin chain, and wherein the first and the second genes are separated by an internal ribosome entry site, and introducing the vector to the host cell under conditions such the first immunoglobulin chain and the second immunoglobulin chain encoded by the first and second exogenous genes are expressed. In some embodiments, the first immunoglobulin chain is an immunoglobulin light chain (*e.g.*, λ or κ) and the second immunoglobulin chain is an immunoglobulin heavy chain (*e.g.*, γ, α, μ, δ, or ε). In other embodiments, the first immunoglobulin chain is an immunoglobulin heavy chain (*e.g.*, γ, α, μ, δ, or ε) and the second immunoglobulin chain is an immunoglobulin light chain (*e.g.*, λ or κ). In some embodiments, the vector is a retroviral vector. In other embodiments, the vector further contains a bovine α-lactalbumin signal peptide. In still further embodiments, the vector further contains a bovine/human hybrid α-lactalbumin promoter. In yet other embodiments, the first immunoglobulin chain and the second immunoglobulin chain are expressed at a ratio of about 0.9:1.1 to 1:1. The present invention also provides immunoglobulins produced by the methods described herein. The present invention is not limited to the use of any particular vector. Indeed, it is contemplated that a variety of vectors find use in the present invention, including, but not limited to

plasmid and retroviral vectors. In some preferred embodiments, the retroviral vector is pseudotyped.

In still further embodiments, the present invention provides methods of indirectly detecting the expression of a protein of interest comprising providing a host cell transduced or transfected with a vector encoding a polycistronic sequence, wherein the polycistronic sequence comprises a signal protein and a protein of interest operably linked by an IRES, and culturing the host cells under conditions such that the signal protein and protein of interest are produced, wherein the presence of the signal protein indicates the presence of the protein of interest. The methods of the present invention are not limited to the expression of any particular protein of interest. Indeed, the expression of a variety of proteins of interest is contemplated, including, but not limited to, G-protein coupled receptors. The present invention is not limited to the use of any particular signal protein. Indeed, the use of variety of signal proteins is contemplated, including, but not limited to, immunoglobulin heavy and light chains, beta-galactosidase, beta-lactamase, green fluorescent protein, and luciferase. In particularly preferred embodiments, expression of the signal protein and protein of interest is driven by the same promoter and the signal protein and protein of interest are transcribed as a single transcriptional unit.

DESCRIPTION OF THE FIGURES

Figure 1 is a Western blot of a 15% SDS-PAGE gel run under denaturing conditions and probed with anti-human IgG (Fc) and anti-human IgG (kappa).

Figure 2 is a graph of MN14 expression over time.

Figure 3 is a Western blot of a 15% PAGE run under non-denaturing conditions and probed with anti-human IgG (Fc) and anti-human IgG (Kappa).

Figure 4 provides the sequence for the hybrid human-bovine alpha-lactalbumin promoter (SEQ ID NO:1).

Figure 5 provides the sequence for the mutated PPE sequence (SEQ ID NO:2).

Figure 6 provides the sequence for the IRES-Signal peptide sequence (SEQ ID NO:3).

Figures 7a and 7b provide the sequence for CMV MN14 vector (SEQ ID NO:4).

Figures 8a and 8b provide the sequence for the CMV LL2 vector (SEQ ID NO:5).

Figures 9a-c provide the sequence for the MMTV MN14 vector (SEQ ID NO:6).

Figures 10a-d provide the sequence for the alpha-lactalbumin MN14 Vector (SEQ ID NO:7).

Figures 11a-c provide the sequence for the alpha-lactalbumin Bot vector (SEQ ID NO:8).

Figures 12a-b provide the sequence for the LSRNL vector (SEQ ID NO:9).

Figures 13a-b provide the sequence for the alpha-lactalbumin cc49IL2 vector (SEQ ID NO:10).

Figures 14a-c provides the sequence for the alpha-lactalbumin YP vector (SEQ ID NO:11).

Figure 15 provides the sequence for the IRES-Casein signal peptide sequence (SEQ ID NO:12).

Figures 16a-c provide the sequence for the LNBOTDC vector (SEQ ID NO:13).

Figures 17a-d provide the sequence of a retroviral vector that expresses a G-Protein coupled receptor and antibody light chain.

DEFINITIONS

To facilitate understanding of the invention, a number of terms are defined below.

As used herein, the term "host cell" refers to any eukaryotic cell (*e.g.*, mammalian cells, avian cells, amphibian cells, plant cells, fish cells, and insect cells), whether located *in vitro* or *in vivo*.

As used herein, the term "cell culture" refers to any *in vitro* culture of cells. Included within this term are continuous cell lines (*e.g.*, with an immortal phenotype), primary cell cultures, finite cell lines (*e.g.*, non-transformed cells), and any other cell population maintained *in vitro*, including oocytes and embryos.

As used herein, the term "vector" refers to any genetic element, such as a plasmid, phage, transposon, cosmid, chromosome, virus, virion, etc., which is capable of replication when associated with the proper control elements and which can transfer gene sequences between cells. Thus, the term includes cloning and expression vehicles, as well as viral vectors.

As used herein, the term "integrating vector" refers to a vector whose integration or insertion into a nucleic acid (*e.g.*, a chromosome) is accomplished via an integrase. Examples of "integrating vectors" include, but are not limited to, retroviral vectors, transposons, and adeno associated virus vectors.

As used herein, the term "integrated" refers to a vector that is stably inserted into the genome (*i.e.*, into a chromosome) of a host cell.

As used herein, the term "multiplicity of infection" or "MOI" refers to the ratio of integrating vectors:host cells used during transfection or transduction of host cells. For example, if 1,000,000 vectors are used to transduce 100,000 host cells, the multiplicity of infection is 10. The use of this term is not limited to events involving transduction, but instead encompasses introduction of a vector into a host by methods such as lipofection, microinjection, calcium phosphate precipitation, and electroporation.

As used herein, the term "genome" refers to the genetic material (*e.g.*, chromosomes) of an organism.

The term "nucleotide sequence of interest" refers to any nucleotide sequence (*e.g.*, RNA or DNA), the manipulation of which may be deemed desirable for any reason (*e.g.*, treat disease, confer improved qualities, expression of a protein of interest in a host cell, *etc.*), by one of ordinary skill in the art. Such nucleotide sequences include, but are not limited to, coding sequences of structural genes (*e.g.*, reporter genes, selection marker genes, oncogenes, drug resistance genes, growth factors, *etc.*), and non-coding regulatory sequences which do not encode an mRNA or protein product (*e.g.*, promoter sequence, polyadenylation sequence, termination sequence, enhancer sequence, *etc.*).

As used herein, the term "protein of interest" refers to a protein encoded by a nucleic acid of interest.

As used herein, the term "signal protein" refers to a protein that is co-expressed with a protein of interest and which, when detected by a suitable assay, provides indirect evidence of expression of the protein of interest. Examples of signal protein useful in the present invention include, but are not limited to, immunoglobulin heavy and light chains, beta-galactosidase, beta-lactamase, green fluorescent protein, and luciferase.

As used herein, the term "exogenous gene" refers to a gene that is not naturally

present in a host organism or cell, or is artificially introduced into a host organism or cell.

The term "gene" refers to a nucleic acid (*e.g.*, DNA or RNA) sequence that comprises coding sequences necessary for the production of a polypeptide or precursor (*e.g.*, proinsulin). The polypeptide can be encoded by a full length coding sequence or by any portion of the coding sequence so long as the desired activity or functional properties (*e.g.*, enzymatic activity, ligand binding, signal transduction, etc.) of the full-length or fragment are retained. The term also encompasses the coding region of a structural gene and includes sequences located adjacent to the coding region on both the 5' and 3' ends for a distance of about 1 kb or more on either end such that the gene corresponds to the length of the full-length mRNA. The sequences that are located 5' of the coding region and which are present on the mRNA are referred to as 5' untranslated sequences. The sequences that are located 3' or downstream of the coding region and which are present on the mRNA are referred to as 3' untranslated sequences. The term "gene" encompasses both cDNA and genomic forms of a gene. A genomic form or clone of a gene contains the coding region interrupted with non-coding sequences termed "introns" or "intervening regions" or "intervening sequences." Introns are segments of a gene which are transcribed into nuclear RNA (hnRNA); introns may contain regulatory elements such as enhancers. Introns are removed or "spliced out" from the nuclear or primary transcript; introns therefore are absent in the messenger RNA (mRNA) transcript. The mRNA functions during translation to specify the sequence or order of amino acids in a nascent polypeptide.

As used herein, the term "gene expression" refers to the process of converting genetic information encoded in a gene into RNA (*e.g.*, mRNA, rRNA, tRNA, or snRNA) through "transcription" of the gene (*i.e.*, via the enzymatic action of an RNA polymerase), and for protein encoding genes, into protein through "translation" of mRNA. Gene expression can be regulated at many stages in the process. "Up-regulation" or "activation" refers to regulation that increases the production of gene expression products (*i.e.*, RNA or protein), while "down-regulation" or "repression" refers to regulation that decrease production. Molecules (*e.g.*, transcription factors) that are involved in up-regulation or down-regulation are often called "activators" and "repressors," respectively.

Where "amino acid sequence" is recited herein to refer to an amino acid sequence of a

naturally occurring protein molecule, "amino acid sequence" and like terms, such as "polypeptide" or "protein" are not meant to limit the amino acid sequence to the complete, native amino acid sequence associated with the recited protein molecule.

As used herein, the terms "nucleic acid molecule encoding," "DNA sequence encoding," "DNA encoding," "RNA sequence encoding," and "RNA encoding" refer to the order or sequence of deoxyribonucleotides or ribonucleotides along a strand of deoxyribonucleic acid or ribonucleic acid. The order of these deoxyribonucleotides or ribonucleotides determines the order of amino acids along the polypeptide (protein) chain. The DNA or RNA sequence thus codes for the amino acid sequence.

As used herein, the term "variant," when used in reference to a protein, refers to proteins encoded by partially homologous nucleic acids so that the amino acid sequence of the proteins varies. As used herein, the term "variant" encompasses proteins encoded by homologous genes having both conservative and nonconservative amino acid substitutions that do not result in a change in protein function, as well as proteins encoded by homologous genes having amino acid substitutions that cause decreased (*e.g.*, null mutations) protein function or increased protein function.

As used herein, the terms "complementary" or "complementarity" are used in reference to polynucleotides (*i.e.,* a sequence of nucleotides) related by the base-pairing rules. For example, for the sequence "A-G-T," is complementary to the sequence "T-C-A." Complementarity may be "partial," in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be "complete" or "total" complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, as well as detection methods that depend upon binding between nucleic acids.

The terms "homology" and "percent identity" when used in relation to nucleic acids refers to a degree of complementarity. There may be partial homology (*i.e.*, partial identity) or complete homology (*i.e.*, complete identity). A partially complementary sequence is one that at least partially inhibits a completely complementary sequence from hybridizing to a target nucleic acid sequence and is referred to using the functional term "substantially

homologous." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or Northern blot, solution hybridization and the like) under conditions of low stringency. A substantially homologous sequence or probe (*i.e.*, an oligonucleotide which is capable of hybridizing to another oligonucleotide of interest) will compete for and inhibit the binding (*i.e.*, the hybridization) of a completely homologous sequence to a target sequence under conditions of low stringency. This is not to say that conditions of low stringency are such that non-specific binding is permitted; low stringency conditions require that the binding of two sequences to one another be a specific (*i.e.*, selective) interaction. The absence of non-specific binding may be tested by the use of a second target which lacks even a partial degree of complementarity (*e.g.*, less than about 30% identity); in the absence of non-specific binding the probe will not hybridize to the second non-complementary target.

The art knows well that numerous equivalent conditions may be employed to comprise low stringency conditions; factors such as the length and nature (DNA, RNA, base composition) of the probe and nature of the target (DNA, RNA, base composition, present in solution or immobilized, etc.) and the concentration of the salts and other components (*e.g.*, the presence or absence of formamide, dextran sulfate, polyethylene glycol) are considered and the hybridization solution may be varied to generate conditions of low stringency hybridization different from, but equivalent to, the above listed conditions. In addition, the art knows conditions that promote hybridization under conditions of high stringency (*e.g.*, increasing the temperature of the hybridization and/or wash steps, the use of formamide in the hybridization solution, etc.).

When used in reference to a double-stranded nucleic acid sequence such as a cDNA or genomic clone, the term "substantially homologous" refers to any probe that can hybridize to either or both strands of the double-stranded nucleic acid sequence under conditions of low stringency as described above.

When used in reference to a single-stranded nucleic acid sequence, the term "substantially homologous" refers to any probe that can hybridize (*i.e.*, it is the complement of) the single-stranded nucleic acid sequence under conditions of low stringency as described

above.

As used herein, the term "hybridization" is used in reference to the pairing of complementary nucleic acids. Hybridization and the strength of hybridization (*i.e.*, the strength of the association between the nucleic acids) is impacted by such factors as the degree of complementary between the nucleic acids, stringency of the conditions involved, the T_m of the formed hybrid, and the G:C ratio within the nucleic acids. A single molecule that contains pairing of complementary nucleic acids within its structure is said to be "self-hybridized."

As used herein, the term "T_m" is used in reference to the "melting temperature" of a nucleic acid. The melting temperature is the temperature at which a population of double-stranded nucleic acid molecules becomes half dissociated into single strands. The equation for calculating the T_m of nucleic acids is well known in the art. As indicated by standard references, a simple estimate of the T_m value may be calculated by the equation: $T_m = 81.5 + 0.41(\% G + C)$, when a nucleic acid is in aqueous solution at 1 M NaCl (*See e.g.,* Anderson and Young, Quantitative Filter Hybridization, *in Nucleic Acid Hybridization* [1985]). Other references include more sophisticated computations that take structural as well as sequence characteristics into account for the calculation of T_m.

As used herein the term "stringency" is used in reference to the conditions of temperature, ionic strength, and the presence of other compounds such as organic solvents, under which nucleic acid hybridizations are conducted. With "high stringency" conditions, nucleic acid base pairing will occur only between nucleic acid fragments that have a high frequency of complementary base sequences. Thus, conditions of "weak" or "low" stringency are often required with nucleic acids that are derived from organisms that are genetically diverse, as the frequency of complementary sequences is usually less.

"High stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 \cdot H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 μg/ml denatured salmon sperm DNA followed by washing in a solution comprising 0.1X SSPE, 1.0% SDS at 42°C when a probe of about 500 nucleotides in length is employed.

"Medium stringency conditions" when used in reference to nucleic acid hybridization comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 \cdot H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.5% SDS, 5X Denhardt's reagent and 100 μg/ml denatured salmon sperm DNA followed by washing in a solution comprising 1.0X SSPE, 1.0% SDS at 42°C when a probe of about 500 nucleotides in length is employed.

"Low stringency conditions" comprise conditions equivalent to binding or hybridization at 42°C in a solution consisting of 5X SSPE (43.8 g/l NaCl, 6.9 g/l $NaH_2PO_4 \cdot H_2O$ and 1.85 g/l EDTA, pH adjusted to 7.4 with NaOH), 0.1% SDS, 5X Denhardt's reagent [50X Denhardt's contains per 500 ml: 5 g Ficoll (Type 400, Pharamcia), 5 g BSA (Fraction V; Sigma)] and 100 μg/ml denatured salmon sperm DNA followed by washing in a solution comprising 5X SSPE, 0.1% SDS at 42°C when a probe of about 500 nucleotides in length is employed.

A gene may produce multiple RNA species that are generated by differential splicing of the primary RNA transcript. cDNAs that are splice variants of the same gene will contain regions of sequence identity or complete homology (representing the presence of the same exon or portion of the same exon on both cDNAs) and regions of complete non-identity (for example, representing the presence of exon "A" on cDNA 1 wherein cDNA 2 contains exon "B" instead). Because the two cDNAs contain regions of sequence identity they will both hybridize to a probe derived from the entire gene or portions of the gene containing sequences found on both cDNAs; the two splice variants are therefore substantially homologous to such a probe and to each other.

The terms "in operable combination," "in operable order," and "operably linked" as used herein refer to the linkage of nucleic acid sequences in such a manner that a nucleic acid molecule capable of directing the transcription of a given gene and/or the synthesis of a desired protein molecule is produced. The term also refers to the linkage of amino acid sequences in such a manner so that a functional protein is produced.

As used herein, the term "selectable marker" refers to a gene that encodes an enzymatic activity that confers the ability to grow in medium lacking what would otherwise be an essential nutrient (*e.g.* the *HIS3* gene in yeast cells); in addition, a selectable marker

may confer resistance to an antibiotic or drug upon the cell in which the selectable marker is expressed. Selectable markers may be "dominant"; a dominant selectable marker encodes an enzymatic activity that can be detected in any eukaryotic cell line. Examples of dominant selectable markers include the bacterial aminoglycoside 3' phosphotransferase gene (also referred to as the *neo* gene) that confers resistance to the drug G418 in mammalian cells, the bacterial hygromycin G phosphotransferase (*hyg*) gene that confers resistance to the antibiotic hygromycin and the bacterial xanthine-guanine phosphoribosyl transferase gene (also referred to as the *gpt* gene) that confers the ability to grow in the presence of mycophenolic acid. Other selectable markers are not dominant in that their use must be in conjunction with a cell line that lacks the relevant enzyme activity. Examples of non-dominant selectable markers include the thymidine kinase (*tk*) gene that is used in conjunction with *tk*$^-$ cell lines, the CAD gene which is used in conjunction with CAD-deficient cells and the mammalian hypoxanthine-guanine phosphoribosyl transferase (*hprt*) gene which is used in conjunction with *hprt*$^-$ cell lines. A review of the use of selectable markers in mammalian cell lines is provided in Sambrook, J. *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, New York (1989) pp.16.9-16.15.

As used herein, the term "regulatory element" refers to a genetic element which controls some aspect of the expression of nucleic acid sequences. For example, a promoter is a regulatory element that facilitates the initiation of transcription of an operably linked coding region. Other regulatory elements are splicing signals, polyadenylation signals, termination signals, RNA export elements, internal ribosome entry sites, etc. (defined *infra*).

Transcriptional control signals in eukaryotes comprise "promoter" and "enhancer" elements. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription (Maniatis *et al.*, Science 236:1237 [1987]). Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in yeast, insect and mammalian cells, and viruses (analogous control elements, *i.e.*, promoters, are also found in prokaryotes). The selection of a particular promoter and enhancer depends on what cell type is to be used to express the protein of interest. Some eukaryotic promoters and enhancers have a broad host range while others are functional in a limited subset of cell types (for review see, Voss *et al.*, Trends Biochem. Sci.,

11:287 [1986]; and Maniatis *et al.*, *supra*). For example, the SV40 early gene enhancer is very active in a wide variety of cell types from many mammalian species and has been widely used for the expression of proteins in mammalian cells (Dijkema *et al.*, EMBO J. 4:761 [1985]). Two other examples of promoter/enhancer elements active in a broad range of mammalian cell types are those from the human elongation factor 1α gene (Uetsuki *et al.*, J. Biol. Chem., 264:5791 [1989]; Kim *et al.*, Gene 91:217 [1990]; and Mizushima and Nagata, Nuc. Acids. Res., 18:5322 [1990]) and the long terminal repeats of the Rous sarcoma virus (Gorman *et al.*, Proc. Natl. Acad. Sci. USA 79:6777 [1982]) and the human cytomegalovirus (Boshart *et al.*, Cell 41:521 [1985]).

As used herein, the term "promoter/enhancer" denotes a segment of DNA which contains sequences capable of providing both promoter and enhancer functions (*i.e.*, the functions provided by a promoter element and an enhancer element, see above for a discussion of these functions). For example, the long terminal repeats of retroviruses contain both promoter and enhancer functions. The enhancer/promoter may be "endogenous" or "exogenous" or "heterologous." An "endogenous" enhancer/promoter is one which is naturally linked with a given gene in the genome. An "exogenous" or "heterologous" enhancer/promoter is one which is placed in juxtaposition to a gene by means of genetic manipulation (*i.e.*, molecular biological techniques such as cloning and recombination) such that transcription of that gene is directed by the linked enhancer/promoter.

Regulatory elements may be tissue specific or cell specific. The term "tissue specific" as it applies to a regulatory element refers to a regulatory element that is capable of directing selective expression of a nucleotide sequence of interest to a specific type of tissue (*e.g.*, liver) in the relative absence of expression of the same nucleotide sequence of interest in a different type of tissue (*e.g.*, lung).

Tissue specificity of a regulatory element may be evaluated by, for example, operably linking a reporter gene to a promoter sequence (which is not tissue-specific) and to the regulatory element to generate a reporter construct, introducing the reporter construct into the genome of an animal such that the reporter construct is integrated into every tissue of the resulting transgenic animal, and detecting the expression of the reporter gene (*e.g.*, detecting mRNA, protein, or the activity of a protein encoded by the reporter gene) in different tissues

of the transgenic animal. The detection of a greater level of expression of the reporter gene in one or more tissues relative to the level of expression of the reporter gene in other tissues shows that the regulatory element is "specific" for the tissues in which greater levels of expression are detected. Thus, the term "tissue-specific" (*e.g.*, liver-specific) as used herein is a relative term that does not require absolute specificity of expression. In other words, the term "tissue-specific" does not require that one tissue have extremely high levels of expression and another tissue have no expression. It is sufficient that expression is greater in one tissue than another. By contrast, "strict" or "absolute" tissue-specific expression is meant to indicate expression in a single tissue type (*e.g.*, liver) with no detectable expression in other tissues.

The term "cell type specific" as applied to a regulatory element refers to a regulatory element which is capable of directing selective expression of a nucleotide sequence of interest in a specific type of cell in the relative absence of expression of the same nucleotide sequence of interest in a different type of cell within the same tissue. The term "cell type specific" when applied to a regulatory element also means a regulatory element capable of promoting selective expression of a nucleotide sequence of interest in a region within a single tissue.

Cell type specificity of a regulatory element may be assessed using methods well known in the art (*e.g.*, immunohistochemical staining and/or Northern blot analysis). Briefly, for immunohistochemical staining, tissue sections are embedded in paraffin, and paraffin sections are reacted with a primary antibody specific for the polypeptide product encoded by the nucleotide sequence of interest whose expression is regulated by the regulatory element. A labeled (*e.g.*, peroxidase conjugated) secondary antibody specific for the primary antibody is allowed to bind to the sectioned tissue and specific binding detected (*e.g.*, with avidin/biotin) by microscopy. Briefly, for Northern blot analysis, RNA is isolated from cells and electrophoresed on agarose gels to fractionate the RNA according to size followed by transfer of the RNA from the gel to a solid support (*e.g.*, nitrocellulose or a nylon membrane). The immobilized RNA is then probed with a labeled oligo-deoxyribonucleotide probe or DNA probe to detect RNA species complementary to the probe used. Northern blots are a standard tool of molecular biologists.

The term "promoter," "promoter element," or "promoter sequence" as used herein, refers to a DNA sequence which when ligated to a nucleotide sequence of interest is capable

of controlling the transcription of the nucleotide sequence of interest into mRNA. A promoter is typically, though not necessarily, located 5' (*i.e.*, upstream) of a nucleotide sequence of interest whose transcription into mRNA it controls, and provides a site for specific binding by RNA polymerase and other transcription factors for initiation of transcription.

Promoters may be constitutive or regulatable. The term "constitutive" when made in reference to a promoter means that the promoter is capable of directing transcription of an operably linked nucleic acid sequence in the absence of a stimulus (*e.g.*, heat shock, chemicals, *etc.*). In contrast, a "regulatable" promoter is one which is capable of directing a level of transcription of an operably linked nucleic acid sequence in the presence of a stimulus (*e.g.*, heat shock, chemicals, *etc.*) which is different from the level of transcription of the operably linked nucleic acid sequence in the absence of the stimulus.

The presence of "splicing signals" on an expression vector often results in higher levels of expression of the recombinant transcript. Splicing signals mediate the removal of introns from the primary RNA transcript and consist of a splice donor and acceptor site (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, New York [1989], pp. 16.7-16.8). A commonly used splice donor and acceptor site is the splice junction from the 16S RNA of SV40.

Efficient expression of recombinant DNA sequences in eukaryotic cells requires expression of signals directing the efficient termination and polyadenylation of the resulting transcript. Transcription termination signals are generally found downstream of the polyadenylation signal and are a few hundred nucleotides in length. The term "poly A site" or "poly A sequence" as used herein denotes a DNA sequence that directs both the termination and polyadenylation of the nascent RNA transcript. Efficient polyadenylation of the recombinant transcript is desirable as transcripts lacking a poly A tail are unstable and are rapidly degraded. The poly A signal utilized in an expression vector may be "heterologous" or "endogenous." An endogenous poly A signal is one that is found naturally at the 3' end of the coding region of a given gene in the genome. A heterologous poly A signal is one that is isolated from one gene and placed 3' of another gene. A commonly used heterologous poly A signal is the SV40 poly A signal. The SV40 poly A signal is contained on a 237 bp *Bam*HI/*Bcl*I restriction fragment and directs both termination and polyadenylation (Sambrook,

supra, at 16.6-16.7).

Eukaryotic expression vectors may also contain "viral replicons "or "viral origins of replication." Viral replicons are viral DNA sequences that allow for the extrachromosomal replication of a vector in a host cell expressing the appropriate replication factors. Vectors that contain either the SV40 or polyoma virus origin of replication replicate to high "copy number" (up to 10^4 copies/cell) in cells that express the appropriate viral T antigen. Vectors that contain the replicons from bovine papillomavirus or Epstein-Barr virus replicate extrachromosomally at "low copy number" (~100 copies/cell). However, it is not intended that expression vectors be limited to any particular viral origin of replication.

As used herein, the term "long terminal repeat" of "LTR" refers to transcriptional control elements located in or isolated from the U3 region 5' and 3' of a retroviral genome. As is known in the art, long terminal repeats may be used as control elements in retroviral vectors, or isolated from the retroviral genome and used to control expression from other types of vectors.

As used herein, the term "secretion signal" refers to any DNA sequence which when operably linked to a recombinant DNA sequence encodes a signal peptide which is capable of causing the secretion of the recombinant polypeptide. In general, the signal peptides comprise a series of about 15 to 30 hydrophobic amino acid residues (*See, e.g.*, Zwizinski *et al.*, J. Biol. Chem. 255(16): 7973-77 [1980], Gray *et al.*, Gene 39(2): 247-54 [1985], and Martial *et al.*, Science 205: 602-607 [1979]). Such secretion signal sequences are preferably derived from genes encoding polypeptides secreted from the cell type targeted for tissue-specific expression (*e.g.*, secreted milk proteins for expression in and secretion from mammary secretory cells). Secretory DNA sequences, however, are not limited to such sequences. Secretory DNA sequences from proteins secreted from many cell types and organisms may also be used (*e.g.*, the secretion signals for t-PA, serum albumin, lactoferrin, and growth hormone, and secretion signals from microbial genes encoding secreted polypeptides such as from yeast, filamentous fungi, and bacteria).

As used herein, the terms "RNA export element" or "Pre-mRNA Processing Enhancer (PPE)" refer to 3' and 5' cis-acting post-transcriptional regulatory elements that enhance export of RNA from the nucleus. "PPE" elements include, but are not limited to Mertz

sequences (described in U.S. Pat. Nos. 5,914,267 and 5,686,120, all of which are incorporated herein by reference) and woodchuck mRNA processing enhancer (WPRE; WO99/14310 and U.S. Pat. No. 6,136,597, each of which is incorporated herein by reference).

As used herein, the term "polycistronic" refers to an mRNA encoding more than polypeptide chain (*See, e.g.*, WO 93/03143, WO 88/05486, and European Pat. No. 117058, all of which are incorporated herein by reference). Likewise, the term "arranged in polycistronic sequence" refers to the arrangement of genes encoding two different polypeptide chains in a single mRNA.

As used herein, the term "internal ribosome entry site" or "IRES" refers to a sequence located between polycistronic genes that permits the production of the expression product originating from the second gene by internal initiation of the translation of the dicistronic mRNA. Examples of internal ribosome entry sites include, but are not limited to, those derived from foot and mouth disease virus (FDV), encephalomyocarditis virus, poliovirus and RDV (Scheper *et al.*, Biochem. 76: 801-809 [1994]; Meyer *et al.*, J. Virol. 69: 2819-2824 [1995]; Jang *et al.*, 1988, J. Virol. 62: 2636-2643 [1998]; Haller *et al.*, J. Virol. 66: 5075-5086 [1995]). Vectors incorporating IRES's may be assembled as is known in the art. For example, a retroviral vector containing a polycistronic sequence may contain the following elements in operable association: nucleotide polylinker, gene of interest, an internal ribosome entry site and a mammalian selectable marker or another gene of interest. The polycistronic cassette is situated within the retroviral vector between the 5' LTR and the 3' LTR at a position such that transcription from the 5' LTR promoter transcribes the polycistronic message cassette. The transcription of the polycistronic message cassette may also be driven by an internal promoter (*e.g.*, cytomegalovirus promoter) or an inducible promoter, which may be preferable depending on the use. The polycistronic message cassette can further comprise a cDNA or genomic DNA (gDNA) sequence operatively associated within the polylinker. Any mammalian selectable marker can be utilized as the polycistronic message cassette mammalian selectable marker. Such mammalian selectable markers are well known to those of skill in the art and can include, but are not limited to, kanamycin/G418, hygromycin B or mycophenolic acid resistance markers.

As used herein, the term "retrovirus" refers to a retroviral particle which is capable of

entering a cell (*i.e.*, the particle contains a membrane-associated protein such as an envelope protein or a viral G glycoprotein which can bind to the host cell surface and facilitate entry of the viral particle into the cytoplasm of the host cell) and integrating the retroviral genome (as a double-stranded provirus) into the genome of the host cell. The term "retrovirus" encompasses Oncovirinae (*e.g.*, Moloney murine leukemia virus (MoMOLV), Moloney murine sarcoma virus (MoMSV), and Mouse mammary tumor virus (MMTV), Spumavirinae, amd Lentivirinae (*e.g.*, Human immunodeficiency virus, Simian immunodeficiency virus, Equine infection anemia virus, and Caprine arthritis-encephalitis virus; *See, e.g.*, U.S. Pat. Nos. 5,994,136 and 6,013,516, both of which are incorporated herein by reference).

As used herein, the term "retroviral vector" refers to a retrovirus that has been modified to express a gene of interest. Retroviral vectors can be used to transfer genes efficiently into host cells by exploiting the viral infectious process. Foreign or heterologous genes cloned (*i.e.*, inserted using molecular biological techniques) into the retroviral genome can be delivered efficiently to host cells which are susceptible to infection by the retrovirus. Through well known genetic manipulations, the replicative capacity of the retroviral genome can be destroyed. The resulting replication-defective vectors can be used to introduce new genetic material to a cell but they are unable to replicate. A helper virus or packaging cell line can be used to permit vector particle assembly and egress from the cell. Such retroviral vectors comprise a replication-deficient retroviral genome containing a nucleic acid sequence encoding at least one gene of interest (*i.e.*, a polycistronic nucleic acid sequence can encode more than one gene of interest), a 5' retroviral long terminal repeat (5' LTR); and a 3' retroviral long terminal repeat (3' LTR).

The term "pseudotyped retroviral vector" refers to a retroviral vector containing a heterologous membrane protein. The term "membrane-associated protein" refers to a protein (*e.g.*, a viral envelope glycoprotein or the G proteins of viruses in the Rhabdoviridae family such as VSV, Piry, Chandipura and Mokola) which are associated with the membrane surrounding a viral particle; these membrane-associated proteins mediate the entry of the viral particle into the host cell. The membrane associated protein may bind to specific cell surface protein receptors, as is the case for retroviral envelope proteins or the membrane-associated protein may interact with a phospholipid component of the plasma membrane of the host cell,

as is the case for the G proteins derived from members of the Rhabdoviridae family.

The term "heterologous membrane-associated protein" refers to a membrane-associated protein which is derived from a virus which is not a member of the same viral class or family as that from which the nucleocapsid protein of the vector particle is derived. "Viral class or family" refers to the taxonomic rank of class or family, as assigned by the International Committee on Taxonomy of Viruses.

The term "Rhabdoviridae" refers to a family of enveloped RNA viruses that infect animals, including humans, and plants. The Rhabdoviridae family encompasses the genus Vesiculovirus which includes vesicular stomatitis virus (VSV), Cocal virus, Piry virus, Chandipura virus, and Spring viremia of carp virus (sequences encoding the Spring viremia of carp virus are available under GenBank accession number U18101). The G proteins of viruses in the Vesiculovirus genera are virally-encoded integral membrane proteins that form externally projecting homotrimeric spike glycoproteins complexes that are required for receptor binding and membrane fusion. The G proteins of viruses in the Vesiculovirus genera have a covalently bound palmititic acid (C_{16}) moiety. The amino acid sequences of the G proteins from the Vesiculoviruses are fairly well conserved. For example, the Piry virus G protein share about 38% identity and about 55% similarity with the VSV G proteins (several strains of VSV are known, *e.g.*, Indiana, New Jersey, Orsay, San Juan, etc., and their G proteins are highly homologous). The Chandipura virus G protein and the VSV G proteins share about 37% identity and 52% similarity. Given the high degree of conservation (amino acid sequence) and the related functional characteristics (*e.g.*, binding of the virus to the host cell and fusion of membranes, including syncytia formation) of the G proteins of the Vesiculoviruses, the G proteins from non-VSV Vesiculoviruses may be used in place of the VSV G protein for the pseudotyping of viral particles. The G proteins of the Lyssa viruses (another genera within the Rhabdoviridae family) also share a fair degree of conservation with the VSV G proteins and function in a similar manner (*e.g.*, mediate fusion of membranes) and therefore may be used in place of the VSV G protein for the pseudotyping of viral particles. The Lyssa viruses include the Mokola virus and the Rabies viruses (several strains of Rabies virus are known and their G proteins have been cloned and sequenced). The Mokola virus G protein shares stretches of homology (particularly over the extracellular and transmembrane

domains) with the VSV G proteins which show about 31% identity and 48% similarity with the VSV G proteins. Preferred G proteins share at least 25% identity, preferably at least 30% identity and most preferably at least 35% identity with the VSV G proteins. The VSV G protein from which New Jersey strain (the sequence of this G protein is provided in GenBank accession numbers M27165 and M21557) is employed as the reference VSV G protein.

As used herein, the term "lentivirus vector" refers to retroviral vectors derived from the Lentiviridae family (*e.g.*, human immunodeficiency virus, simian immunodeficiency virus, equine infectious anemia virus, and caprine arthritis-encephalitis virus) that are capable of integrating into non-dividing cells (*See, e.g.*, U.S. Pat. Nos. 5,994,136 and 6,013,516, both of which are incorporated herein by reference).

The term "pseudotyped lentivirus vector" refers to lentivirus vector containing a heterologous membrane protein *(e.g.*, a viral envelope glycoprotein or the G proteins of viruses in the Rhabdoviridae family such as VSV, Piry, Chandipura and Mokola).

As used herein, the term "transposon" refers to transposable elements (*e.g.*, Tn5, Tn7, and Tn10) that can move or transpose from one position to another in a genome. In general, the transposition is controlled by a transposase. The term "transposon vector," as used herein, refers to a vector encoding a nucleic acid of interest flanked by the terminal ends of transposon. Examples of transposon vectors include, but are not limited to, those described in U.S. Pat. Nos. 6,027,722; 5,958,775; 5,968,785; 5,965,443; and 5,719,055, all of which are incorporated herein by reference.

As used herein, the term "adeno-associated virus (AAV) vector" refers to a vector derived from an adeno-associated virus serotype, including without limitation, AAV-1, AAV-2, AAV-3, AAV-4, AAV-5, AAVX7, etc. AAV vectors can have one or more of the AAV wild-type genes deleted in whole or part, preferably the *rep* and/or *cap* genes, but retain functional flanking ITR sequences.

AAV vectors can be constructed using recombinant techniques that are known in the art to include one or more heterologous nucleotide sequences flanked on both ends (5' and 3') with functional AAV ITRs. In the practice of the invention, an AAV vector can include at least one AAV ITR and a suitable promoter sequence positioned upstream of the heterologous nucleotide sequence and at least one AAV ITR positioned downstream of the heterologous

sequence. A "recombinant AAV vector plasmid" refers to one type of recombinant AAV vector wherein the vector comprises a plasmid. As with AAV vectors in general, 5' and 3' ITRs flank the selected heterologous nucleotide sequence.

AAV vectors can also include transcription sequences such as polyadenylation sites, as well as selectable markers or reporter genes, enhancer sequences, and other control elements which allow for the induction of transcription. Such control elements are described above.

As used herein, the term "AAV virion" refers to a complete virus particle. An AAV virion may be a wild type AAV virus particle (comprising a linear, single-stranded AAV nucleic acid genome associated with an AAV capsid, *i.e.*, a protein coat), or a recombinant AAV virus particle (described below). In this regard, single-stranded AAV nucleic acid molecules (either the sense/coding strand or the antisense/anticoding strand as those terms are generally defined) can be packaged into an AAV virion; both the sense and the antisense strands are equally infectious.

As used herein, the term "recombinant AAV virion" or "rAAV" is defined as an infectious, replication-defective virus composed of an AAV protein shell encapsidating (*i.e.*, surrounding with a protein coat) a heterologous nucleotide sequence, which in turn is flanked 5' and 3' by AAV ITRs. A number of techniques for constructing recombinant AAV virions are known in the art (*See, e.g.*, U.S. Patent No. 5,173,414; WO 92/01070; WO 93/03769; Lebkowski *et al.*, Molec. Cell. Biol. 8:3988-3996 [1988]; Vincent *et al.*, Vaccines 90 [1990] (Cold Spring Harbor Laboratory Press); Carter, Current Opinion in Biotechnology 3:533-539 [1992]; Muzyczka, Current Topics in Microbiol. and Immunol. 158:97-129 [1992]; Kotin, Human Gene Therapy 5:793-801 [1994]; Shelling and Smith, Gene Therapy 1:165-169 [1994]; and Zhou *et al.*, J. Exp. Med. 179:1867-1875 [1994], all of which are incorportaed herein by reference).

Suitable nucleotide sequences for use in AAV vectors (and, indeed, any of the vectors described herein) include any functionally relevant nucleotide sequence. Thus, the AAV vectors of the present invention can comprise any desired gene that encodes a protein that is defective or missing from a target cell genome or that encodes a non-native protein having a desired biological or therapeutic effect (*e.g.*, an antiviral function), or the sequence can correspond to a molecule having an antisense or ribozyme function. Suitable genes include

those used for the treatment of inflammatory diseases, autoimmune, chronic and infectious diseases, including such disorders as AIDS, cancer, neurological diseases, cardiovascular disease, hypercholestemia; various blood disorders including various anemias, thalasemias and hemophilia; genetic defects such as cystic fibrosis, Gaucher's Disease, adenosine deaminase (ADA) deficiency, emphysema, etc. A number of antisense oligonucleotides (*e.g.*, short oligonucleotides complementary to sequences around the translational initiation site (AUG codon) of an mRNA) that are useful in antisense therapy for cancer and for viral diseases have been described in the art. (*See, e.g.*, Han *et al.*, Proc. Natl. Acad. Sci. USA 88:4313-4317 [1991]; Uhlmann *et al.*, Chem. Rev. 90:543-584 [1990]; Helene *et al.*, Biochim. Biophys. Acta. 1049:99-125 [1990]; Agarwal *et al.*, Proc. Natl. Acad. Sci. USA 85:7079-7083 [1989]; and Heikkila *et al.*, Nature 328:445-449 [1987]). For a discussion of suitable ribozymes, *see, e.g.*, Cech *et al.* (1992) J. Biol. Chem. 267:17479-17482 and U.S. Patent No. 5,225,347, incorporated herein by reference.

By "adeno-associated virus inverted terminal repeats" or "AAV ITRs" is meant the art-recognized palindromic regions found at each end of the AAV genome which function together in *cis* as origins of DNA replication and as packaging signals for the virus. For use with the present invention, flanking AAV ITRs are positioned 5' and 3' of one or more selected heterologous nucleotide sequences and, together with the *rep* coding region or the Rep expression product, provide for the integration of the selected sequences into the genome of a target cell.

The nucleotide sequences of AAV ITR regions are known (*See, e.g.*, Kotin, Human Gene Therapy 5:793-801 [1994]; Berns, K.I. "Parvoviridae and their Replication" in Fundamental Virology, 2nd Edition, (B.N. Fields and D.M. Knipe, eds.) for the AAV-2 sequence. As used herein, an "AAV ITR" need not have the wild-type nucleotide sequence depicted, but may be altered, *e.g.*, by the insertion, deletion or substitution of nucleotides. Additionally, the AAV ITR may be derived from any of several AAV serotypes, including without limitation, AAV-1, AAV-2, AAV-3, AAV-4, AAV-5, AAVX7, etc. The 5' and 3' ITRs which flank a selected heterologous nucleotide sequence need not necessarily be identical or derived from the same AAV serotype or isolate, so long as they function as intended, *i.e.*, to allow for the integration of the associated heterologous sequence into the

target cell genome when the *rep* gene is present (either on the same or on a different vector), or when the Rep expression product is present in the target cell.

As used herein the term, the term "*in vitro*" refers to an artificial environment and to processes or reactions that occur within an artificial environment. *In vitro* environments can consist of, but are not limited to, test tubes and cell cultures. The term "*in vivo*" refers to the natural environment (*e.g.*, an animal or a cell) and to processes or reaction that occur within a natural environment.

As used herein, the term "clonally derived" refers to a cell line that it derived from a single cell.

As used herein, the term "non-clonally derived" refers to a cell line that is derived from more than one cell.

As used herein, the term "passage" refers to the process of diluting a culture of cells that has grown to a particular density or confluency (*e.g.*, 70% or 80% confluent), and then allowing the diluted cells to regrow to the particular density or confluency desired (*e.g.*, by replating the cells or establishing a new roller bottle culture with the cells.

As used herein, the term "stable," when used in reference to genome, refers to the stable maintenance of the information content of the genome from one generation to the next, or, in the particular case of a cell line, from one passage to the next. Accordingly, a genome is considered to be stable if no gross changes occur in the genome (*e.g.*, a gene is deleted or a chromosomal translocation occurs). The term "stable" does not exclude subtle changes that may occur to the genome such as point mutations.

As used herein, the term "response," when used in reference to an assay, refers to the generation of a detectable signal (*e.g.*, accumulation of reporter protein, increase in ion concentration, accumulation of a detectable chemical product).

As used herein, the term "membrane receptor protein" refers to membrane spanning proteins that bind a ligand (*e.g.*, a hormone or neurotransmitter). As is known in the art, protein phosphorylation is a common regulatory mechanism used by cells to selectively modify proteins carrying regulatory signals from outside the cell to the nucleus. The proteins that execute these biochemical modifications are a group of enzymes known as protein kinases. They may further be defined by the substrate residue that they target for

phosphorylation. One group of protein kinases are the tyrosine kinases (TKs) which selectively phosphorylate a target protein on its tyrosine residues. Some tyrosine kinases are membrane-bound receptors (RTKs), and, upon activation by a ligand, can autophosphorylate as well as modify substrates. The initiation of sequential phosphorylation by ligand stimulation is a paradigm that underlies the action of such effectors as, for example, epidermal growth factor (EGF), insulin, platelet-derived growth factor (PDGF), and fibroblast growth factor (FGF). The receptors for these ligands are tyrosine kinases and provide the interface between the binding of a ligand (hormone, growth factor) to a target cell and the transmission of a signal into the cell by the activation of one or more biochemical pathways. Ligand binding to a receptor tyrosine kinase activates its intrinsic enzymatic activity (*See, e.g.*, Ullrich and Schlessinger, Cell 61:203-212 [1990]). Tyrosine kinases can also be cytoplasmic, non-receptor-type enzymes and act as a downstream component of a signal transduction pathway.

As used herein, the term "signal transduction protein" refers to a proteins that are activated or otherwise effected by ligand binding to a membrane receptor protein or some other stimulus. Examples of signal transduction protein include adenyl cyclase, phospholipase C, and G-proteins. Many membrane receptor proteins are coupled to G-proteins (*i.e.*, G-protein coupled receptors (GPCRs); for a review, *see* Neer, 1995, Cell 80:249-257 [1995]). Typically, GPCRs contain seven transmembrane domains. Putative GPCRs can be identified on the basis of sequence homology to known GPCRs.

GPCRs mediate signal transduction across a cell membrane upon the binding of a ligand to an extracellular portion of a GPCR. The intracellular portion of a GPCR interacts with a G-protein to modulate signal transduction from outside to inside a cell. A GPCR is therefore said to be "coupled" to a G-protein. G-proteins are composed of three polypeptide subunits: an α subunit, which binds and hydrolyses GTP, and a dimeric $\beta\gamma$ subunit. In the basal, inactive state, the G-protein exists as a heterotrimer of the α and $\beta\gamma$ subunits. When the G-protein is inactive, guanosine diphosphate (GDP) is associated with the α subunit of the G-protein. When a GPCR is bound and activated by a ligand, the GPCR binds to the G-protein heterotrimer and decreases the affinity of the Gα subunit for GDP. In its active state, the G subunit exchanges GDP for guanine triphosphate (GTP) and active Gα subunit

disassociates from both the receptor and the dimeric βγ subunit. The disassociated, active Gα subunit transduces signals to effectors that are "downstream" in the G-protein signalling pathway within the cell. Eventually, the G-protein's endogenous GTPase activity returns active G subunit to its inactive state, in which it is associated with GDP and the dimeric βγ subunit.

Numerous members of the heterotrimeric G-protein family have been cloned, including more than 20 genes encoding various Gα subunits. The various G subunits have been categorized into four families, on the basis of amino acid sequences and functional homology. These four families are termed $G\alpha_s$, $G\alpha_i$, $G\alpha_q$, and $G\alpha_{12}$. Functionally, these four families differ with respect to the intracellular signaling pathways that they activate and the GPCR to which they couple.

For example, certain GPCRs normally couple with $G\alpha_s$ and, through $G\alpha_s$, these GPCRs stimulate adenylyl cyclase activity. Other GPCRs normally couple with $GG\alpha_q$, and through $GG\alpha_q$, these GPCRs can activate phospholipase C (PLC), such as the β isoform of phospholipase C (*i.e.*, PLCβ, Stermweis and Smrcka, Trends in Biochem. Sci. 17:502-506 [1992]).

As used herein, the term "immunoglobulin" refers to proteins which bind a specific antigen. Immunoglobulins include, but are not limited to, polyclonal, monoclonal, chimeric, and humanized antibodies, Fab fragments, F(ab')2 fragments, and includes immunoglobulins of the following classes: IgG, IgA, IgM, IgD, IbE, and secreted immunoglobulins (sIg). Immunoglobulins generally comprise two identical heavy chains (γ, α, μ, δ, or ε) and two light chains (κ or λ).

As used herein, the term "antigen binding protein" refers to proteins which bind to a specific antigen. "Antigen binding proteins" include, but are not limited to, immunoglobulins, including polyclonal, monoclonal, chimeric, and humanized antibodies; Fab fragments, F(ab')2 fragments, and Fab expression libraries; and single chain antibodies. Various procedures known in the art are used for the production of polyclonal antibodies. For the production of an antibody, various host animals can be immunized by injection with the peptide corresponding to the desired epitope including but not limited to rabbits, mice, rats, sheep, goats, etc. In a preferred embodiment, the peptide is conjugated to an immunogenic carrier

(*e.g.*, diphtheria toxoid, bovine serum albumin (BSA), or keyhole limpet hemocyanin (KLH)). Various adjuvants are used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (Bacille Calmette-Guerin) and *Corynebacterium parvum*.

For preparation of monoclonal antibodies, any technique that provides for the production of antibody molecules by continuous cell lines in culture may be used (*See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press,* Cold Spring Harbor, NY). These include, but are not limited to, the hybridoma technique originally developed by Köhler and Milstein (Köhler and Milstein, Nature 256:495-497 [1975]), as well as the trioma technique, the human B-cell hybridoma technique (*See e.g.,* Kozbor *et al.* Immunol. Today 4:72 [1983]), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al., in Monoclonal Antibodies and Cancer Therapy,* Alan R. Liss, Inc., pp. 77-96 [1985]).

According to the invention, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778; herein incorporated by reference) can be adapted to produce specific single chain antibodies as desired. An additional embodiment of the invention utilizes the techniques known in the art for the construction of Fab expression libraries (Huse *et al.,* Science 246:1275-1281 [1989]) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

Antibody fragments that contain the idiotype (antigen binding region) of the antibody molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')2 fragment that can be produced by pepsin digestion of an antibody molecule; the Fab' fragments that can be generated by reducing the disulfide bridges of an F(ab')2 fragment, and the Fab fragments that can be generated by treating an antibody molecule with papain and a reducing agent.

Genes encoding antigen binding proteins can be isolated by methods known in the art. In the production of antibodies, screening for the desired antibody can be accomplished by

techniques known in the art (*e.g.*, radioimmunoassay, ELISA (enzyme-linked immunosorbant assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), Western Blots, precipitation reactions, agglutination assays (*e.g.*, gel agglutination assays, hemagglutination assays, etc.), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc.) etc.

As used herein, the term "reporter gene" refers to a gene encoding a protein that may be assayed. Examples of reporter genes include, but are not limited to, luciferase (*See, e.g.*, deWet *et al.*, Mol. Cell. Biol. 7:725 [1987] and U.S. Pat Nos.,6,074,859; 5,976,796; 5,674,713; and 5,618,682; all of which are incorporated herein by reference), green fluorescent protein (*e.g.*, GenBank Accession Number U43284; a number of GFP variants are commercially available from CLONTECH Laboratories, Palo Alto, CA), chloramphenicol acetyltransferase, β-galactosidase, alkaline phosphatase, and horse radish peroxidase.

As used herein, the term "purified" refers to molecules, either nucleic or amino acid sequences, that are removed from their natural environment, isolated or separated. An "isolated nucleic acid sequence" is therefore a purified nucleic acid sequence. "Substantially purified" molecules are at least 60% free, preferably at least 75% free, and more preferably at least 90% free from other components with which they are naturally associated.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel regulatory sequences for use in expression vectors. In some embodiments, the present invention provides retroviral expression vectors containing novel regulatory elements. In addition, in still other embodiments, the present invention provides methods for expressing proteins of interest in host cells. In particularly preferred embodiments, the present invention provides methods for expressing two chains of a multisubunit protein (*e.g.*, a heavy chain and a light chain of an immunoglobulin or the subunits of follicle stimulating hormone) in a nearly equal ratio. These methods take advantage of the novel regulatory sequences and vectors of the present invention to solve problems in the prior art.

I. Components of Retroviral Expression Vectors

In particularly preferred embodiments, the retroviral vectors of the present invention include the following elements in operable association: a) a 5' LTR; b) a packaging signal; c) a 3' LTR, and d) a nucleic acid encoding a protein of interest located between the 5' and 3' LTRs. In addition, in some preferred embodiments, novel compositions, including, but not limited to those described below are included in expression vectors in order to aid in the expression, secretion and purification of proteins of interest. The following novel elements are described in more detail below: bovine/human hybrid alpha-lactalbumin (α-LA) promoter (A); mutant RNA export element (B); and internal ribosome entry site (C).

A. Bovine/Human Hybrid Alpha Lactalbumin Promoter

In some embodiments, the present invention provides a hybrid α-lactalbumin (α-LA) promoter. It is contemplated that the hybrid promoter may be constructed from portions of any two or more mammalian α-lactalbumin promoters (*e.g.*, human, bovine, goat, sheep, rabbit, or mouse α-lactalbumin promoters among others; *see, e.g.*, GenBank Accession numbers AF124257; AF123893; AX067504; Soulier *et al.*, Transgenic Res. 8(1):23-31 (1999); McKee *et al.*, Nat. Biotech. 16(7):647-51 (1998); Lubon *et al.*, Biochem. J. 256(2):391-6 (1988); and U.S. Pat. No. 5,530,177). In some embodiments, the portion of at least one of the promoters contributing to the hybrid is at least 50 nucleotides in length, while in preferred embodiments, the portion of at least one of the promoters contributing to the hybrid is at least 100 nucleotides in length, while in particularly preferred embodiments, the portion of at least one of the promoters contributing to the hybrid is at least 500 nucleotides length, with the portion of the at least one other promoter contributing to the hybrid being of similar or longer length. Once constructed, the hybrid promoters can be assayed for functionality by operably linking the promoter to a reporter gene such as beta-galactosidase, green fluorescent protein, or luciferase, creating a transgenic animal such as transgenic mouse or bovine that comprises the resulting construct, and assaying various tissues of the resulting transgenic animal to determine the specificity of expression from the hybrid promoter. In preferred embodiments, expression from the hybrid promoter is substantially specific to the mammary gland, and in particular to mammary epithelial cells, with no or only trace levels of expression of in other

tissues.

In particularly preferred embodiments, the hybrid promoter is a bovine/human hybrid α-lactalbumin (α-LA) promoter (SEQ ID NO: 1). The human portion of the promoter was derived from human genomic DNA and contains bases from +15 relative to the transcription start point to –600 relative to the transcription start point. The bovine portion is attached to the end of the human portion and corresponds to bases -550 to -2000 relative to the transcription start point.

The hybrid promoter preferably used in the present invention utilizes a region of the human promoter that contained an internal poly-adenylation signal. The internal poly-adenylation signal was removed by mutation. The mutation was at base 2012 and involved a change from A to T. The present invention is not limited to any particular mechanism of action. Indeed, an understanding of the mechanism is not required to practice the present invention. Nevertheless, it is contemplated the removal of poly-adenylation signals improves retroviral RNA production by eliminating premature mRNA termination problems. In addition, it is contemplated that additional enhancer regions exist in the human, but not the bovine sequence. The hybrid promoter was constructed to take advantage of these additional sequences. Likewise, the hybrid promoter contains bovine elements that may or may not be found in the human promoter.

B. RNA Export Element

In some embodiments, the present invention comprises a mutant RNA export element (pre-mRNA processing element (PPE), Mertz sequence, or WPRE; *See, e.g.*, U.S. Pat. Nos. 5,914,267 and 5,686,120 and PCT Publication WO99/14310, all of which are incorporated herein by reference). The present invention is not limited to any particular mechanism of action. Indeed, an understanding of the mechanism is not required to practice the present invention. Nevertheless, it is contemplated that the use of RNA export elements allows or facilitates high levels of expression of the protein of interest without incorporating splice signals or introns in the nucleic acid sequence encoding the protein of interest.

In some embodiments, a mutated PPE element is utilized. In some particularly preferred embodiments, the PPE sequence is mutated to remove internal ATG sequences. The

present invention is not limited to any particular mechanism of action. Indeed, an understanding of the mechanism is not required to practice the present invention. Nevertheless, it is contemplated that the removal of internal start sequences prevents potential unwanted translation initiation. In some embodiments utilizing a mutated PPE sequence, bases 4, 112, 131, and 238 of SEQ ID NO: 2 were changed from a G to a T. In all cases, these changes resulted in and ATG start codon being mutated to an ATT codon. In some embodiments, the mutated PPE sequence is placed in the 5' untranslated region (UTR) of the mRNA encoding the gene of interest. In other embodiments, the mutated PPE sequence is placed in the 3' UTR of the mRNA encoding the gene of interest. In some preferred embodiments, two mutated PPE sequences separated by a linker are placed in a head to tail array (*See e.g.*, SEQ ID NO:2) . It has been shown that two copies of the sequence cause a more dramatic effect on mRNA export. In other embodiments, 2-20 copies of the mutated PPE sequence are placed in the mRNA encoding the gene of interest.

Functional variants of the above sequences are easily identified by operably linking the variant sequence to a test gene in a vector, transfecting a host cell with the vector, and analyzing the host cell for expression of the test gene. Suitable test genes, host cells, and vectors are disclosed in the examples.

C. Internal Ribosome Entry Site

In some embodiments, the present invention comprises an internal ribosome entry site (IRES)/signal peptide sequence (*e.g.*, SEQ ID NOs:3 and 12). The present invention contemplates that a variety of signal sequences may be fused with a variety of IRES sequences. Suitable signal sequences include those from α-lactalbumin, casein, tissue plasminogen activator, serum albumin, lactoferrin, and lactoferrin (*See, e.g.*, Zwizinski *et al.*, J. Biol. Chem. 255(16): 7973-77 [1980], Gray *et al.*, Gene 39(2): 247-54 [1985], and Martial *et al.*, Science 205: 602-607 [1979]). Such secretion signal sequences are preferably derived from genes encoding polypeptides secreted from the cell type targeted for tissue-specific expression (*e.g.*, secreted milk proteins for expression in and secretion from mammary secretory cells). Suitable IRES sequences include, but are not limited, to those derived from foot and mouth disease virus (FDV), encephalomyocarditis virus, poliovirus and RDV

(Scheper *et al.*, Biochem. 76: 801-809 [1994]; Meyer *et al.*, J. Virol. 69: 2819-2824 [1995]; Jang *et al.*, 1988, J. Virol. 62: 2636-2643 [1998]; Haller *et al.*, J. Virol. 66: 5075-5086 [1995]). Functional IRES/signal peptide sequences may be identified by operably linking two genes with the sequence and an appropriate promoter, transfecting a host cell with the construct, and assaying the host cell for production the proteins encoding by the two genes. Suitable genes, vector constructs, and host cells for such screening are provided in the examples. In preferred embodiments, the coding sequences for the IRES and signal peptide are adjacent to one another, with no intervening coding sequences (*i.e.*, that may be separated by noncoding sequences in some instances).

The present invention is not limited to any particular mechanism of action. Indeed, an understanding of the mechanism is not required to practice the present invention. The IRES allows translation of the gene to start at the IRES sequence, thereby resulting in the expression of two genes of interest in the same construct. The bovine α-lactalbumin signal peptide or casein signal peptide causes extracellular secretion of expressed protein products.

In some embodiments, the initial ATG of the signal peptide is attached to the IRES in order to allow the most efficient translation initiation from the IRES. In some embodiments, the second codon of the signal peptide is mutated from an ATG to a GCC, changing the second amino acid of the α-lactalbumin signal peptide from a methionine to an alanine. The present invention is not limited to any particular mechanism of action. Indeed, an understanding of the mechanism is not required to practice the present invention. Nevertheless, it is contemplated that this mutation facilitates more efficient translation initiation by the IRES. In some embodiments, the (IRES)/signal peptide is inserted into a vector between two genes of interest. In these embodiments, the (IRES)/signal peptide creates a second translation initiation site, allowing for the expression of two polypeptides from the same expression vector. In other words, a single transcript is produced that encodes two different polypeptides (*e.g.*, the heavy and light chains of an immunoglobulin).

In some embodiments, the signal peptide is derived from α-lactalbumin. In other embodiments, the present invention comprises an internal ribosome entry site (IRES)/modified bovine α-S1 Casein signal peptide fusion protein (SEQ ID NO:12). The present invention is not limited to any particular mechanism of action. Indeed, an understanding of the

mechanism is not required to practice the present invention. The IRES allows translation of the gene to start at the IRES sequence, allowing the expression of two genes of interest in the same construct. The bovine α-S1 casein signal peptide causes secretion of expressed protein products.

In some embodiments the second codon of the bovine α-S1 casein signal peptide is mutated from a AAA to a GCC. The mutation results in the second codon of the signal peptide being changed from an alanine to a lysine. In some embodiments, the third codon of the signal peptide is mutated from a CTT to a TTG, a change which does not result and an amino acid substitution. The present invention is not limited to any particular mechanism of action. Indeed, an understanding of the mechanism is not required to practice the present invention. Nevertheless, it is contemplated that this mutation allows more efficient translation initiation by the IRES.

II. Retroviral Expression Vectors

In some embodiments, the present invention comprises retroviral expression vectors. Retroviruses (family Retroviridae) are generally divided into three groups: the spumaviruses (*e.g.*, human foamy virus); the lentiviruses (*e.g.*, human immunodeficiency virus and sheep visna virus), and the oncoviruses (*e.g.*, MLV and Rous sarcoma virus).

Retroviruses are enveloped (*i.e.*, surrounded by a host cell-derived lipid bilayer membrane) single-stranded RNA viruses which infect animal cells. When a retrovirus infects a cell, its RNA genome is converted into a double-stranded linear DNA form (*i.e.*, it is reverse transcribed). The DNA form of the virus is then integrated into the host cell genome as a provirus. The provirus serves as a template for the production of additional viral genomes and viral mRNAs. Mature viral particles containing two copies of genomic RNA bud from the surface of the infected cell. The viral particle comprises the genomic RNA, reverse transcriptase and other *pol* gene products inside the viral capsid (containing the viral *gag* gene products) which is surrounded by a lipid bilayer membrane derived from the host cell containing the viral envelope glycoproteins (also referred to as membrane-associated proteins).

The genomic organization of numerous retroviruses is well known to the art and this

has allowed the adaptation of the retroviral genome to produce retroviral vectors. The production of a recombinant retroviral vector carrying a gene of interest is typically achieved in two stages.

First, the gene of interest is inserted into a retroviral vector which contains the sequences necessary for the efficient expression of the gene of interest (including promoter and/or enhancer elements which may be provided by the viral long terminal repeats (LTRs) or by an internal promoter/enhancer and relevant splicing signals), sequences required for the efficient packaging of the viral RNA into infectious virions (*e.g.*, the packaging signal (Psi), the tRNA primer binding site (-PBS), the 3' regulatory sequences required for reverse transcription (+PBS)) and the viral LTRs. The LTRs contain sequences required for the association of viral genomic RNA, reverse transcriptase and integrase functions, and sequences involved in directing the expression of the genomic RNA to be packaged in viral particles. For safety reasons, many recombinant retroviral vectors lack functional copies of the genes which are essential for viral replication (these essential genes are either deleted or disabled); therefore, the resulting virus is said to be "replication defective".

Second, following the construction of the recombinant vector, the vector DNA is introduced into a packaging cell line. Packaging cell lines provide viral proteins required in *trans* for the packaging of the viral genomic RNA into viral particles having the desired host range (*i.e.*, the viral-encoded gag, pol and env proteins). The host range is controlled, in part, by the type of envelope gene product expressed on the surface of the viral particle. Packaging cell lines may express ecotrophic, amphotropic or xenotropic envelope gene products. Alternatively, the packaging cell line may lack sequences encoding a viral envelope (env) protein. In this case the packaging cell line will package the viral genome into particles lacking a membrane-associated protein (*e.g.*, an env protein). In order to produce viral particles containing a membrane associated protein which will permit entry of the virus into a cell, the packaging cell line containing the retroviral sequences is commonly transfected with sequences encoding a membrane-associated protein (*e.g.*, the G protein of vesicular stomatitis virus (VSV)). The transfected packaging cell will then produce viral particles which contain the membrane-associated protein expressed by the transfected packaging cell line; these viral particles which contain viral genomic RNA derived from one virus encapsidated by the

envelope proteins of another virus are said to be "pseudotyped virus particles".

The retroviral vectors of the present invention can be further modified to include additional regulatory sequences. As described above, the retroviral vectors of the present invention include the following elements in operable association: a) a 5' LTR; b) a packaging signal; c) a 3' LTR; and d) a nucleic acid encoding a protein of interest located between the 5' and 3' LTRs. In some embodiments of the present invention, the nucleic acid of interest may be arranged in opposite orientation to the 5' LTR when transcription from an internal promoter is desired. Suitable internal promoters include, but are not limited to, the alpha-lactalbumin promoter, the CMV promoter, and the thymidine kinase promoter.

In other embodiments of the present invention, where secretion of the protein of interest is desired, the vectors are modified by including a signal peptide sequence in operable association with the protein of interest. The sequences of several suitable signal peptides are known in the art, including, but not limited to, those derived from tissue plasminogen activator, human growth hormone, lactoferrin, alpha S1-casein, and alpha-lactalbumin.

In other embodiments of the present invention, the vectors are modified by incorporating one or more of the elements described above, including, but not limited to, an RNA export element, a PPE element, and an IRES/bovine α-lactalbumin signal sequence.

The retroviral vectors of the present invention may further comprise a selectable marker which facilitates selection of transformed cells. A number of selectable markers known in the art find use in the present invention, including, but not limited to the bacterial aminoglycoside 3' phosphotransferase gene (also referred to as the "*neo* gene") that confers resistance to the drug G418 in mammalian cells, the bacterial hygromycin G phosphotransferase (*hyg*) gene that confers resistance to the antibiotic hygromycin, and the bacterial xanthine-guanine phosphoribosyl transferase gene (also referred to as the "*gpt* gene") that confers the ability to grow in the presence of mycophenolic acid. In some embodiments, the selectable marker gene is provided as part of a polycistronic sequence also encoding the protein of interest.

In still other embodiments of the present invention, the retroviral vectors may comprise recombination elements recognized by a recombination system (*e.g.*, the cre/loxP or flp recombinase systems: *See, e.g.*, Hoess *et al.*, Nucleic Acids Res., 14:2287 [1986], O'Gorman

et al., Science 251:1351 [1991], van Deursen *et al.*, Proc. Natl. Acad. Sci. USA 92:7376 [1995], and U.S. Pat. No. 6,025,192, incorporated herein by reference). After integration of the vectors into the genome of the host cell, the host cell can be transiently transfected (*e.g.*, by electroporation, lipofection, or microinjection) with either a recombinase enzyme (*e.g.*, Cre recombinase) or a nucleic acid sequence encoding the recombinase enzyme and one or more nucleic acid sequences encoding a protein of interest flanked by sequences recognized by the recombination enzyme so that the nucleic acid sequence of interest is inserted into the integrated vector.

Viral vectors, including recombinant retroviral vectors, provide a more efficient means of transferring genes into cells, as compared to other techniques such as calcium phosphate-DNA co-precipitation or DEAE-dextran-mediated transfection, electroporation or microinjection of nucleic acids. Nonetheless, the present invention is not limited to any particular mechanism. Indeed, an understanding of the mechanism is not required to practice the present invention. Nevertheless, it is believed that the efficiency of viral transfer is due in part to the fact that the transfer of nucleic acid is a receptor-mediated process (*i.e.*, the virus binds to a specific receptor protein on the surface of the target cell). In addition, once inside a cell, the virally transferred nucleic acid integrates in controlled manner. This is in contrast to nucleic acids transferred by other means (*e.g.*, calcium phosphate-DNA co-precipitation), which are typically subject to rearrangement and degradation.

Example 1, below, describes several illustrative examples of retroviral vectors of the current invention. However, it is not intended that the present invention be limited to the vectors described in Example 1. Indeed, any suitable retroviral vectors containing the novel elements of the present invention are contemplated. Furthermore, the elements described above find use in other vectors such as AAV vectors, transposon vectors, plasmids, bacterial artificial chromosomes, and yeast artificial chromosomes.

III. Expression of Proteins

In some embodiments of the present invention, the vectors and regulatory elements described above find use in the expression of one or more proteins. The present invention is not limited to the production of any particular protein. Indeed, the production of a wide

variety of proteins is contemplated, including, but not limited to, erythropoietin, alpha-interferon, alpha-1 proteinase inhibitor, angiogenin, antithrombin III, beta-acid decarboxylase, human growth hormone, bovine growth hormone, porcine growth hormone, human serum albumin, beta-interferon, calf intestine alkaline phosphatase, cystic fibrosis transmembrane regulator, Factor VIII, Factor IX, Factor X, insulin, lactoferrin, tissue plasminogen activator, myelin basic protein, insulin, proinsulin, prolactin, hepatitis B antigen, immunoglobulins, monoclonal antibody CTLA4 Ig, Tag 72 monoclonal antibody, Tag 72 single chain antigen binding protein, protein C, cytokines and their receptors (*e.g.*, tumor necrosis factor alpha and beta), growth hormone releasing factor, parathyroid hormone, thyroid stimulating hormone, lipoproteins, alpha-1-antitrypsin, follicle stimulating hormone, calcitonin, luteinizing hormone, glucagon, von Willebrands factor, atrial natriuretic factor, lung surfactant, urokinase, bombesin, thrombin, hemopoietic growth factor, enkephalinase, human macrophage inflammatory protein (MIP-1-alpha), serum albumins (*e.g.*, mullerian-inhibiting substance), relaxin A-chain, relaxin B-chain, prorelaxin, mouse gonadotropin-associated peptide, beta-lactamase, DNase, inhibin, activin, vascular endothelial growth factor (VEGF), receptors for hormones or growth factors, integrin, protein A or D, rheumatoid factors, neurotrophic factors (*e.g.*, bone-derived neurotrophic factor (BDNF)), neurotrophin-3, -4, -5, or -6 (NT-3, NT-4, NT-5, or NT-6), nerve growth factors (*e.g.*, NGF-beta), platelet-derived growth factor (PDGF), fibroblast growth factors (*e.g.*, aFGF and bFGF), epidermal growth factor (EGF), transforming growth factor (TGF) (*e.g.*, TGF-alpha and TGF-beta, including TGF-β1, TGF-β2, TGF-β3, TGF-β4, or TGF-β5), insulin-like growth factor-I and -II (IGF-I and IGF-II), des(1-3)-IGF-I (brain IGF-I), insulin like growth factor binding proteins; CD proteins (*e.g.*, CD-3, CD-4, CD-8, and CD-19), osteoinductive factors, immunotoxins, bone morphogenetic protein (BMP); interferons (*e.g.*, interferon-alpha, -beta, and -gamma), colony stimulating factors (CSFs) (*e.g.*, M-CSF, GM-CSF, and G-CSF), interleukins (IL) (*e.g.*, IL-1 to IL-10), superoxide dismutase, T-cell receptors, surface membrane proteins, decay accelerating factor, viral antigens (*e.g.*, a portion of the AIDS envelope), transport proteins, homing receptors, addressins, regulatory proteins, antibodies, chimeric proteins (*e.g.*, immunoadhesins), and fragments of any of the above-listed polypeptides. One skilled in the art recognizes that the nucleic acid sequences for these proteins and their homologs are

available from public databases (*e.g.*, Gen Bank).

In some embodiments, the vectors of the present invention are used to express more than one exogenous protein. For example, host cells may be transfected with vectors encoding different proteins of interest (*e.g.*, cotransfection with one vector encoding a first protein of interest and a second vector encoding a second protein of interest). In other embodiments, more than one protein is expressed by arranging the nucleic acids encoding the different proteins of interest in a polycistronic sequence (*e.g.*, bicistronic or tricistronic sequences). This arrangement is especially useful when expression of the different proteins of interest in a 1:1 molar ratio is desired (*e.g.*, expression of the light and heavy chains of an immunoglobulin molecule).

A. Expression of Protein in Cell Culture

In some embodiments of the present invention, proteins are expressed in cell culture. In some embodiments, retroviral vectors are used to express protein in mammalian tissue culture host cells, including, but not limited to, rat fibroblast cells, bovine kidney cells, and human kidney cells, while in some preferred embodiments, protein is expressed in bovine mammary cells. The host cells are cultured according to methods known in the art; suitable culture conditions for mammalian cells are well known in the art (*See e.g.*, J. Immunol. Methods 56:221 [1983], *Animal Cell Culture: A Practical Approach 2nd Ed.*, Rickwood, D. and Hames, B. D., eds. Oxford University Press, New York [1992]).

The present invention contemplates the transfection of a variety of host cells with integrating vectors. A number of mammalian host cell lines are known in the art. In general, these host cells are capable of growth and survival when placed in either monolayer culture or in suspension culture in a medium containing the appropriate nutrients and growth factors, as is described in more detail below. Typically, the cells are capable of expressing and secreting large quantities of a particular protein of interest into the culture medium. Examples of suitable mammalian host cells include, but are not limited to Chinese hamster ovary cells (CHO-K1, ATCC CCl-61); bovine mammary epithelial cells (ATCC CRL 10274; bovine mammary epithelial cells); monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in

suspension culture; *see, e.g.*, Graham *et al.*, J. Gen Virol., 36:59 [1977]); baby hamster kidney cells (BHK, ATCC CCL 10); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23:243-251 [1980]); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather *et al.*, Annals N.Y. Acad. Sci., 383:44-68 [1982]); MRC 5 cells; FS4 cells; rat fibroblasts (208F cells); MDBK cells (bovine kidney cells); and a human hepatoma line (Hep G2).

In addition to mammalian cell lines, the present invention also contemplates the transfection of plant protoplasts with integrating vectors at a low or high multiplicity of infection. For example, the present invention contemplates a plant cell or whole plant comprising at least one integrated integrating vector, preferably a retroviral vector, and most preferably a pseudotyped retroviral vector. All plants that can be produced by regeneration from protoplasts can also be transfected using the process according to the invention (*e.g.*, cultivated plants of the genera *Solanum*, *Nicotiana*, *Brassica*, *Beta*, *Pisum*, *Phaseolus*, *Glycine*, *Helianthus*, *Allium*, *Avena*, *Hordeum*, *Oryzae*, *Setaria*, *Secale*, *Sorghum*, *Triticum*, *Zea*, *Musa*, *Cocos*, *Cydonia*, *Pyrus*, *Malus*, *Phoenix*, *Elaeis*, *Rubus*, *Fragaria*, *Prunus*, *Arachis*, *Panicum*, *Saccharum*, *Coffea*, *Camellia*, *Ananas*, *Vitis* or *Citrus*). In general, protoplasts are produced in accordance with conventional methods (*See, e.g.*, U.S. Pat. Nos. 4,743,548; 4,677,066, 5,149,645; and 5,508,184; all of which are incorporated herein by reference). Plant tissue may be dispersed in an appropriate medium having an appropriate osmotic potential (*e.g.*, 3 to 8 wt. % of a sugar polyol) and one or more polysaccharide hydrolases (*e.g.*, pectinase, cellulase, etc.), and the cell wall degradation allowed to proceed for a sufficient time to provide protoplasts. After filtration the protoplasts may be isolated by centrifugation and may then be resuspended for subsequent treatment or use. Regeneration of protoplasts kept in culture to whole plants is performed by methods known in the art (*See, e.g.*, Evans *et al.*, *Handbook of Plant Cell Culture*, 1: 124-176, MacMillan Publishing Co., New York [1983]; Binding, *Plant Protoplasts*, p. 21-37, CRC Press, Boca Raton [1985],) and Potrykus and Shillito, *Methods in Enzymology*, Vol. 118, Plant Molecular Biology, A. and H.

Weissbach eds., Academic Press, Orlando [1986]).

The present invention also contemplates the use of amphibian and insect host cell lines. Examples of suitable insect host cell lines include, but are not limited to, mosquito cell lines (*e.g.*, ATCC CRL-1660). Examples of suitable amphibian host cell lines include, but are not limited to, toad cell lines (*e.g.*, ATCC CCL-102).

In preferred embodiments of the present invention, the host cell cultures are prepared in a medium suitable for the particular cell being cultured. Commercially available media such as Ham's F10 (Sigma, St. Louis, MO), Minimal Essential Medium (MEM, Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium (DMEM, Sigma) are exemplary nutrient solutions. Suitable media are also described in U.S. Pat. Nos. 4,767,704; 4,657,866; 4,927,762; 5,122,469 and U.S. Pat. No. 4,560,655; and PCT Publications WO 90/03430; and WO 87/00195 (each of which are incorporated herein by reference). Any of these media may be supplemented as necessary, with hormones and/or other growth factors (*e.g.*, insulin, transferrin, or epidermal growth factor), salts (*e.g.*, sodium chloride, calcium, magnesium, and phosphate), buffers (*e.g.*, HEPES), nucleosides (*e.g.*, adenosine and thymidine), antibiotics (*e.g.*, gentamycin (gentamicin)), trace elements (*i.e.*, inorganic compounds usually present at final concentrations in the micromolar range) lipids (*e.g.*, linoleic or other fatty acids) and their suitable carriers, and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations known to those skilled in the art. For mammalian cell culture, the osmolality of the culture medium is generally about 290-330 mOsm.

The present invention also contemplates the use of a variety of culture systems (*e.g.*, petri dishes, 96 well plates, roller bottles, and bioreactors) for the growth and expression of host cells. For example, the host cells can be cultured in a perfusion system. Perfusion culture refers to providing a continuous flow of culture medium through a culture maintained at high cell density. The cells are suspended and do not require a solid support upon which to grow. Generally, fresh nutrients must be supplied continuously with concomitant removal of toxic metabolites and, ideally, selective removal of dead cells. Filtering, entrapment and micro-capsulation methods are all suitable for refreshing the culture environment at sufficient rates.

In alternative embodiments, a fed batch culture procedure is employed. In the preferred fed batch culture method the mammalian host cells and culture medium are supplied to a culturing vessel initially and additional culture nutrients are fed, continuously or in discrete increments, to the culture during culturing, with or without periodic cell and/or product harvest before termination of culture. In some embodiments, the fed batch culture is a semi-continuous fed batch culture in which the whole culture (including cells and medium) is removed from the growth vessel and replaced by fresh medium. Fed batch culture is distinguished from simple batch culture in which all components for cell culturing (including the cells and all culture nutrients) are supplied to the culturing vessel at the start of the culturing process. Fed batch culture can be further distinguished from perfusion culturing insofar as the supernate is not removed from the culturing vessel during the process (in perfusion culturing, the cells are restrained in the culture (*e.g.*, by filtration, encapsulation, anchoring to microcarriers etc.) and the culture medium is continuously or intermittently introduced and removed from the culturing vessel).

Further, the cells of the culture may be propagated according to any scheme or routine suitable for the particular host cell and the particular production plan contemplated. Therefore, the present invention contemplates single step, as well as multiple step culture procedures. In a single step culture, the host cells are inoculated into a culture environment and the processes of the instant invention are employed during a single production phase of the cell culture. In the multi-stage culture procedure, cells are cultivated in a number of steps or phases. For instance, cells may be grown in a first step or growth phase culture wherein cells, possibly removed from storage, are inoculated into a medium suitable for promoting growth and high viability. The cells may be maintained in the growth phase for a suitable period of time by the addition of fresh medium to the host cell culture.

Fed batch or continuous cell culture conditions are contemplated in order to enhance growth of the mammalian cells in the growth phase of the cell culture. In the growth phase, cells are grown under conditions and for a period of time that is optimized for growth. Culture conditions, such as temperature, pH, dissolved oxygen (dO_2) and the like, are those used with the particular host and are apparent to the ordinarily skilled artisan. Generally, the pH is adjusted to a level between about 6.5 and 7.5 using either an acid (*e.g.*, CO_2) or a base

(*e.g.*, Na_2CO_3 or NaOH). A suitable temperature range for culturing mammalian cells (*e.g.*, CHO cells) is between about 30° to 38° C and a suitable dO_2 is between 5-90% of air saturation.

Following the polypeptide production phase, the polypeptide of interest is recovered from the culture medium using well-established techniques. Preferably, the protein of interest is recovered from the culture medium as a secreted polypeptide (*e.g.*, the secretion of the protein of interest is directed by a signal peptide sequence), although it also may be recovered from host cell lysates. As a first step, the culture medium or lysate is centrifuged to remove particulate cell debris. The polypeptide is then purified from contaminant soluble proteins and polypeptides using any suitable method. Suitable purificaiton methods include, but are not limited to fractionation on immunoaffinity or ion-exchange columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using (*e.g.*, Sephadex G-75); and protein A Sepharose columns to remove contaminants such as IgG. A protease inhibitor such as phenyl methyl sulfonyl fluoride (PMSF) also may be useful to inhibit proteolytic degradation during purification. Additionally, the protein of interest can be fused in frame to a marker sequence which allows for purification of the protein of interest. Non-limiting examples of marker sequences include a hexahistidine tag which may be supplied by a vector, preferably a pQE-9 vector, and a hemagglutinin (HA) tag. The HA tag corresponds to an epitope derived from the influenza hemagglutinin protein (*See e.g.*, Wilson *et al.*, Cell, 37:767 [1984]). One skilled in the art appreciates that purification methods suitable for the polypeptide of interest may require modification to account for changes in the character of the polypeptide upon expression in recombinant cell culture.

B. Expression of Proteins in Animals

In some embodiments of the present invention, the host cell utilized for expression of the protein of interest is part of a mammal. In preferred embodiments, the mammal is a transgenic bovine. The transgenic bovine may be produced by any suitable method (*See e.g.*, Chan *et al.*, PNAS, 95:14028 [1998]; U.S. Patent 5,741,957 (incorporated herein by reference); and Pursel *et al.*, Science, 244:1281 [1989]). In particularly preferred

embodiments, the protein is expressed in the mammary gland of a bovine and secreted in the milk of the bovine. In embodiments where proteins are expressed in the milk of a bovine, proteins and signal sequences for tissue specific expression and secretion are utilized, including, but not limited to, bovine/human α-lactalbumin promoter and bovine α-lactalbumin signal sequence. The protein of interest may be recovered from bovine milk using any suitable method, including but not limited to, those described above for the recovery of protein from cell cultures.

Those skilled in the art recognize that the vectors of the present invention will find use in the production of other transgenic animals as well, including, but not limited to, mice, goats, pigs, birds and rabbits (*See e.g.*, U.S Pat. Nos. 5,523,226; 5,453,457; 4,873,191; 4,736,866; each of which is herein incorporated by reference).

C. Expression of Antibodies

In some embodiments of the present invention, single vectors are utilized for the expression of two or more proteins, including individual subunits of multisubunit proteins. In some embodiments, two or more chains of an immunoglobulin (*e.g.*, one heavy chain ((γ, α, μ, δ, or ε) and one light chain (κ or λ)), separated by an IRES sequence, are expressed from the same vector as single transcriptional unit. The present invention is not limited to any particular vector. Indeed, the use of a variety of vectors is contemplated, including, but not limited to plasmids, cosmids, bacterial artificial chomosomes, yeast artificial chromosomes, adeno-associated virus vectors, and adenovirus vectors. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Such vectors include, but are not limited to, the following vectors: 1) Bacterial -- pQE70, pQE60, pQE-9 (Qiagen), pBS, pD10, phagescript, psiX174, pbluescript SK, pBSKS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); and 2) Eukaryotic -- pWLNEO, pSV2CAT, pOG44, PXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, pSVL (Pharmacia). Any other plasmid or vector may be used as long as they are replicable and viable in the host. In some preferred embodiments of the present invention, mammalian expression vectors comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation sites, splice donor and acceptor

sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. In other embodiments, DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

In certain embodiments of the present invention, the DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. Promoters useful in the present invention include, but are not limited to, the LTR or SV40 promoter, the *E. coli lac* or *trp*, the phage lambda P_L and P_R, T3 and T7 promoters, and the cytomegalovirus (CMV) immediate early, herpes simplex virus (HSV) thymidine kinase, and mouse metallothionein-I promoters and other promoters known to control expression of gene in prokaryotic or eukaryotic cells or their viruses. In other embodiments of the present invention, recombinant expression vectors include origins of replication and selectable markers permitting transformation of the host cell (*e.g.*, dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or tetracycline or ampicillin resistance in *E. coli*).

In some embodiments of the present invention, transcription of the DNA encoding the polypeptides of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector. Enhancers are *cis*-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Enhancers useful in the present invention include, but are not limited to, the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

In other embodiments, the expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. In still other embodiments of the present invention, the vector may also include appropriate sequences for amplifying expression.

In some particularly preferred embodiments, retroviral vectors are used to express immunoglobulins. In some embodiments, retroviral vectors for expression of immunoglobulins contain regulatory elements. In some preferred embodiments of the present invention, two immunoglobulins chains are expressed in the same retrovirus vector construct separated by an IRES sequence. In some particularly preferred embodiments, the two chains are separated by an IRES/α-LA signal sequence. In other embodiments, the vector further

contains RNA export elements. In further embodiments, the RNA export element is a WPRE. In still other embodiments, the PPE element is at least one Mertz sequence. In some preferred embodiments, the PPE element is mutated to remove start signals. In other preferred embodiments, two PPE elements are placed in a head to tail array separated by a linker.

In preferred embodiments, expression of immunoglobulins by the vectors of the current invention is controlled by a promoter. In some embodiments, expression is controlled by a CMV promoter, while in other embodiments, expression is controlled by a MMTV promoter. In some preferred embodiments, expression is controlled by a hybrid bovine/human α-LA promoter.

In some embodiments of the present invention, heavy and light chains are expressed by the vectors of the current invention of a ratio of about 0.7:1.3. In preferred embodiments, heavy and light chains are expressed and a ratio of about 0.8:1.2. In particularly preferred embodiments, heavy and light chains are expressed at a ratio of about 0.9:1.1. In still more preferred embodiments, heavy and light chains are expressed at a ratio of about 1:1. In particularly preferred embodiments, the majority (*e.g.*, greater that 90%, preferably greater than 95%, and most preferably greater than about 99%) of the heavy and light chains are correctly assembled in a ratio of 1:1 to form a functional (*e.g.*, able to bind an antigen) antibody.

In illustrative examples of the present invention, immunoglobulins are expressed in a host cell comprising the vectors and elements described above. In some illustrative examples (*See e.g.*, Examples 6, 8, and 12), the vectors described in Example 1 are used to express a variety of immunoglobulins in a variety of cell lines. In general, this expression led to the formation of functional, tetrameric immunoglobulins.

D. Expression of Other Proteins

The vectors of the present invention are also useful for expressing G-protein coupled receptors (GPCRs) and other transmembrane proteins. It is contemplated that when these proteins are expressed, they are correctly inserted into the membrane in their native conformation. Thus, GPCRs and other transmembrane proteins may be purified as part of a

membrane fraction or purified from the membranes by methods known in the art.

Furthermore, the vectors of the present invention are useful for co-expressing a protein of interest for which there is no assay or for which assays are difficult. In this system, a protein of interest and a signal protein are arranged in a polycistronic sequence. Preferably, an IRES sequence separates the signal protein and protein of interest (*e.g.*, a GPCR) and the genes encoding the signal protein and protein of interest are expressed as a single transcriptional unit. The present invention is not limited to any particular signal protein. Indeed, the use of a variety of signal proteins for which easy assays exist is contemplated. These signal proteins include, but are not limited to, green fluorescent protein, luciferase, beta-galactosidase, and antibody heavy or light chains. It is contemplated that when the signal protein and protein of interest are co-expressed from a polycistronic sequence, the presence of the signal protein is indicative of the presence of the protein of interest. Accordingly, in some embodiments, the present invention provides methods for indirectly detecting the expression of protein of interest comprising providing a host cell transfected with a vector encoding a polycistronic sequence, wherein the polycistronic sequence comprises a signal protein and a protein of interest operably linked by an IRES, and culturing the host cells under conditions such that the signal protein and protein of interest are produced, wherein the presence of the signal protein indicates the presence of the protein of interest.

EXPERIMENTAL

The following examples serve to illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

In the experimental disclosure which follows, the following abbreviations apply: M (molar); mM (millimolar); μM (micromolar); nM (nanomolar); mol (moles); mmol (millimoles); μmol (micromoles); nmol (nanomoles); gm (grams); mg (milligrams); μg (micrograms);pg (picograms); L (liters); ml (milliliters); μl (microliters); cm (centimeters); mm (millimeters); μm (micrometers); nm (nanometers); °C (degrees Centigrade); AMP (adenosine 5'-monophosphate); BSA (bovine serum albumin); cDNA (copy or complimentary DNA); CS (calf serum); DNA (deoxyribonucleic acid); ssDNA (single stranded DNA);

dsDNA (double stranded DNA); dNTP (deoxyribonucleotide triphosphate); LH (luteinizing hormone); NIH (National Institutes of Health, Besthesda, MD); RNA (ribonucleic acid); PBS (phosphate buffered saline); *g* (gravity); OD (optical density); HEPES (N-[2-αHydroxyethyl]piperazine-N-[2-ethanesulfonic acid]); HBS (HEPES buffered saline); PBS (phosphate buffered saline); SDS (sodium dodecylsulfate); Tris-HCl (tris[Hydroxymethyl]aminomethane-hydrochloride); Klenow (DNA polymerase I large (Klenow) fragment); rpm (revolutions per minute); EGTA (ethylene glycol-bis(ß-aminoethyl ether) N, N, N', N'-tetraacetic acid); EDTA (ethylenediaminetetracetic acid); bla (ß-lactamase or ampicillin-resistance gene); ORI (plasmid origin of replication); lacI (lac repressor); X-gal (5-bromo-4-chloro-3-indolyl-β-D-galactoside); ATCC (American Type Culture Collection, Rockville, MD); GIBCO/BRL (GIBCO/BRL, Grand Island, NY); Perkin-Elmer (Perkin-Elmer, Norwalk, CT); and Sigam (Sigma Chemical Company, St. Louis, MO).

Example 1

Vector Construction

The following Example describes the construction of vectors used in the experiments below.

A. CMV MN14

The CMV MN14 vector (SEQ ID NO:4; MN14 antibody is described in U.S. Pat. No. 5,874,540, incorporated herein by reference) comprises the following elements, arranged in 5' to 3' order: CMV promoter; MN14 heavy chain signal peptide, MN14 antibody heavy chain; IRES from encephalomyocarditis virus; bovine α-lactalbumin signal peptide; MN 14 antibody light chain; and 3' MoMuLV LTR. In addition to sequences described in SEQ ID NO: 4, the CMV MN14 vector further comprises a 5' MoMuLV LTR, a MoMuLV extended viral packaging signal, and a neomycin phosphotransferase gene (these additional elements are provided in SEQ ID NO:7; the 5' LTR is derived from Moloney Murine Sarcoma Virus in each of the constructs described herein, but is converted to the MoMuLV 5' LTR when integrated).

This construct uses the 5' MoMuLV LTR to control production of the neomycin

phosphotransferase gene. The expression of MN14 antibody is controlled by the CMV promoter. The MN14 heavy chain gene and light chain gene are attached together by an IRES sequence. The CMV promoter drives production of a mRNA containing the heavy chain gene and the light chain gene attached by the IRES. Ribosomes attach to the mRNA at the CAP site and at the IRES sequence. This allows both heavy and light chain protein to be produced from a single mRNA. The mRNA expression from the LTR as well as from the CMV promoter is terminated and poly adenylated in the 3' LTR. The construct was cloned by similar methods as described in section B below.

The IRES sequence (SEQ ID NO:3) comprises a fusion of the IRES from the plasmid pLXIN (Clontech) and the bovine α-lactalbumin signal peptide. The initial ATG of the signal peptide was attached to the IRES to allow the most efficient translation initiation from the IRES. The 3' end of the signal peptide provides a multiple cloning site allowing easy attachment of any protein of interest to create a fusion protein with the signal peptide. The IRES sequence can serve as a translational enhancer as well as creating a second translation initiation site that allows two proteins to be produced from a single mRNA.

The IRES-bovine α-lactalbumin signal peptide was constructed as follows. The portion of the plasmid pLXIN (Clontech, Palo Alto, CA) containing the ECMV IRES was PCR amplified using the following primers.

Primer 1 (SEQ ID NO: 35):
5' GATCCACTAGTAACGGCCGCCAGAATTCGC 3'

Primer 2 (SEQ ID NO: 36):
5' CAGAGAGACAAAGGAGGCCATATTATCATCGTGTTTTTCAAAG 3'

Primer 2 attaches a tail corresponding to the start of the bovine α-lactalbumin signal peptide coding region to the IRES sequence. In addition, the second triplet codon of the α-lactalbumin signal peptide was mutated from ATG to GCC to allow efficient translation from the IRES sequence. This mutation results in a methionine to alanine change in the protein sequence. This mutation was performed because the IRES prefers an alanine as the

second amino acid in the protein chain. The resulting IRES PCR product contains an EcoRI site on the 5' end of the fragment (just downstream of Primer 1 above).

Next, the α-lactalbumin signal peptide containing sequence was PCR amplified from the α-LA Signal Peptide vector construct using the following primers.

Primer 3 (SEQ ID NO: 14):
5' CTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTCTCTG 3'

Primer 4 (SEQ ID NO: 15):
5' TTCGCGAGCTCGAGATCTAGATATCCCATG 3'

Primer 3 attaches a tail corresponding to the 3' end of the IRES sequence to the α-lactalbumin signal peptide coding region. As stated above, the second triplet codon of the bovine α-lactalbumin signal peptide was mutated to allow efficient translation from the IRES sequence. The resulting signal peptide PCR fragment contains NaeI, NcoI, EcoRV, XbaI, BglII and XhoI sites on the 3' end.

After the IRES and signal peptide were amplified individually using the primers shown above, the two reaction products were mixed and PCR was performed using primer 1 and primer 4. The resultant product of this reaction is a spliced fragment that contains the IRES attached to the full length α-lactalbumin signal peptide. The ATG encoding the start of the signal peptide is placed at the same location as the ATG encoding the start of the neomycin phosphotransferase gene found in the vector pLXIN. The fragment also contains the EcoRI site on the 5' end and NaeI, NcoI, EcoRV, XbaI, BglII and XhoI sites on the 3' end.

The spliced IRES/α-lactalbumin signal peptide PCR fragment was digested with EcoRI and XhoI. The α-LA Signal Peptide vector construct was also digested with EcoRI and XhoI. These two fragments were ligated together to give the pIRES construct.

The IRES/α-lactalbumin signal peptide portion of the pIRES vector was sequenced and found to contain mutations in the 5' end of the IRES. These mutations occur in a long stretch of C's and were found in all clones that were isolated.

To repair this problem, pLXIN DNA was digested with EcoRI and BsmFI. The 500bp

band corresponding to a portion of the IRES sequence was isolated. The mutated IRES/α-lactalbumin signal peptide construct was also digested with EcoRI and BsmFI and the mutated IRES fragment was removed. The IRES fragment from pLXIN was then substituted for the IRES fragment of the mutated IRES/α-lactalbumin signal peptide construct. The IRES/α-LA signal peptide portion of resulting plasmid was then verified by DNA sequencing.

The resulting construct was found to have a number of sequence differences when compared to the expected pLXIN sequence obtained from Clontech. We also sequenced the IRES portion of pLXIN purchased from Clontech to verify its sequence. The differences from the expected sequence also appear to be present in the pLXIN plasmid that we obtained from Clontech. Four sequence differences were identified:

bp 347 T - was G in pLXIN sequence

bp 786-788 ACG - was GC in LXIN sequence.

B. CMV LL2

The CMV LL2 (SEQ ID NO:5; LL2 antibody is described in U.S. Pat. No. 6,187,287, incorporated herein by reference) construct comprises the following elements, arranged in 5' to 3' order: 5' CMV promoter (Clontech), LL2 heavy chain signal peptide, LL2 antibody heavy chain; IRES from encephalomyocarditis virus; bovine α-LA signal peptide; LL2 antibody light chain; and 3' MoMuLV LTR. In addition to sequences described in SEQ ID NO:5, the CMV LL2 vector further comprises a 5' MoMuLV LTR, a MoMuLV extended viral packaging signal, and a neomycin phosphotransferase gene (these additional elements are provided in SEQ ID NO:7).

This construct uses the 5' MoMuLV LTR to control production of the neomycin phosphotransferase gene. The expression of LL2 antibody is controlled by the CMV promoter (Clontech). The LL2 heavy chain gene and light chain gene are attached together by an IRES sequence. The CMV promoter drives production of a mRNA containing the heavy chain gene and the light chain gene attached by the IRES. Ribosomes attach to the mRNA at the CAP site and at the IRES sequence. This allows both heavy and light chain protein to be produced from a single mRNA. The mRNA expression from the LTR as well as from the CMV promoter is terminated and poly adenylated in the 3' LTR.

The IRES sequence (SEQ ID NO:3) comprises a fusion of the IRES from the plasmid pLXIN (Clontech) and the bovine alpha-lactalbumin signal peptide. The initial ATG of the signal peptide was attached to the IRES to allow the most efficient translation initiation from the IRES. The 3' end of the signal peptide provides a multiple cloning site allowing easy attachment of any protein of interest to create a fusion protein with the signal peptide. The IRES sequence can serve as a translational enhancer as well as creating a second translation initiation site that allows two proteins to be produced from a single mRNA.

The LL2 light chain gene was attached to the IRES α-lactalbumin signal peptide as follows. The LL2 light chain was PCR amplified from the vector pCRLL2 using the following primers.

Primer 1 (SEQ ID NO: 16):
5' CTACAGGTGTCCACGTCGACATCCAGCTGACCCAG 3'
Primer 2 (SEQ ID NO: 17):
5' CTGCAGAATAGATCTCTAACACTCTCCCCTGTTG 3'

These primers add a HincII site right at the start of the coding region for mature LL2 light chain. Digestion of the PCR product with HincII gives a blunt end fragment starting with the initial GAC encoding mature LL2 on the 5' end. Primer 2 adds a BglII site to the 3' end of the gene right after the stop codon. The resulting PCR product was digested with HincII and BglII and cloned directly into the IRES-Signal Peptide plasmid that was digested with NaeI and BglII.

The Kozak sequence of the LL2 heavy chain gene was then modified. The vector pCRMN14HC was digested with XhoI and AvrII to remove about a 400 bp fragment. PCR was then used to amplify the same portion of the LL2 heavy chain construct that was removed by the XhoI-AvrII digestion. This amplification also mutated the 5' end of the gene to add a better Kozak sequence to the clone. The Kozak sequence was modified to resemble the typical IgG Kozak sequence. The PCR primers are shown below.

Primer 1 (SEQ ID NO: 18):

5'CAGTGTGATCTCGAGAATTCAGGACCTCACCATGGGATGGAGCTGTATCAT 3'

Primer 2 (SEQ ID NO: 19):
5'AGGCTGTATTGGTGGATTCGTCT 3'

The PCR product was digested with XhoI and AvrII and inserted back into the previously digested plasmid backbone.

The "good" Kozak sequence was then added to the light chain gene. The "good" Kozak LL2 heavy chain gene construct was digested with EcoRI and the heavy chain gene containing fragment was isolated. The IRES α-Lactalbumin Signal Peptide LL2 light chain gene construct was also digested with EcoRI. The heavy chain gene was then cloned into the EcoRI site of IRES light chain construct. This resulted in the heavy chain gene being placed at the 5' end of the IRES sequence.

Next, a multiple cloning site was added into the LNCX retroviral backbone plasmid. The LNCX plasmid was digested with HindIII and ClaI. Two oligonucleotide primers were produced and annealed together to create an double stranded DNA multiple cloning site. The following primers were annealed together.

Primer 1 (SEQ ID NO: 20):
5'AGCTTCTCGAGTTAACAGATCTAGGCCTCCTAGGTCGACAT 3'
Primer 2 (SEQ ID NO: 21): 5'
CGATGTCGACCTAGGAGGCCTAGATCTGTTAACTCGAGA 3'

After annealing, the multiple cloning site was ligated into LNCX to create LNC-MCS.

Next, the double chain gene fragment was ligated into the retroviral backbone gene construct. The double chain gene construct created above was digested with SalI and BglII and the double chain containing fragment was isolated. The retroviral expression plasmid LNC-MCS was digested with XhoI and BglII. The double chain fragment was then cloned into the LNC-MCS retroviral expression backbone.

Next, an RNA splicing problem in the construct was corrected. The construct was

digested with NsiI. The resulting fragment was then partially digested with EcoRI. The fragments resulting from the partial digest that were approximately 9300 base pairs in size were gel purified. A linker was created to mutate the splice donor site at the 3' end of the LL2 heavy chain gene. The linker was again created by annealing two oligonucleotide primers together to form the double stranded DNA linker. The two primers used to create the linker are shown below.

Primer 1 (SEQ ID NO: 22):
5'CGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAAAT GAAAGCCG 3'

Primer 2 (SEQ ID NO: 23):
5'AATTCGGCTTTCATTTCCCGGGAGACAGGGAGAGGCTCTTCTGCGTGTAGTGGTTG TGCAGAGCCTCGTGCA 3'

After annealing the linker was substituted for the original NsiI/EcoRI fragment that was removed during the partial digestion.

C. MMTV MN14

The MMTV MN14 (SEQ ID NO:6) construct comprises the following elements, arranged in 5' to 3' order: 5' MMTV promoter; double mutated PPE sequence; MN 14 antibody heavy chain; IRES from encephalomyocarditis virus; bovine αLA signal peptide MN 14 antibody light chain; WPRE sequence; and 3' MoMuLV LTR. In addition to the sequences described in SEQ ID NO:6, the MMTV MN14 vector further comprises a MoMuLV LTR, MoMuLV extended viral packaging signal; neomycin phosphotransferase gene located 5' of the MMTV promoter (these additional elements are provided in SEQ ID NO: 7).

This construct uses the 5' MoMuLV LTR to control production of the neomycin phosphotransferase gene. The expression of MN14 antibody is controlled by the MMTV promoter (Pharmacia). The MN14 heavy chain gene and light chain gene are attached

together by an IRES/ bovine α-LA signal peptide sequence (SEQ ID NO: 3). The MMTV promoter drives production of a mRNA containing the heavy chain gene and the light chain gene attached by the IRES/bovine α-LA signal peptide sequence. Ribosomes attach to the mRNA at the CAP site and at the IRES/ bovine α-LA signal peptide sequence. This allows both heavy and light chain protein to be produced from a single mRNA. In addition, there are two genetic elements contained within the mRNA to aid in export of the mRNA from the nucleus to the cytoplasm and aid in poly-adenylation of the mRNA. The PPE sequence is contained between the RNA CAP site and the start of the MN14 protein coding region, the WPRE is contained between the end of MN14 protein coding and the poly-adenylation site. The mRNA expression from the LTR as well as from the MMTV promoter is terminated and poly-adenylated in the 3' LTR.

ATG sequences within the PPE element (SEQ ID NO:2) were mutated to prevent potential unwanted translation initiation. Two copies of this mutated sequence were used in a head to tail array. This sequence is placed just downstream of the promoter and upstream of the Kozak sequence and signal peptide-coding region. The WPRE is isolated from woodchuck hepatitis virus and also aids in the export of mRNA from the nucleus and creating stability in the mRNA. If this sequence is included in the 3' untranslated region of the RNA, level of protein expression from this RNA increases up to 10-fold.

D. α-LA MN14

The α-LA MN14 (SEQ ID NO:7) construct comprises the following elements, arranged in 5' to 3' order: 5' MoMuLV LTR, MoMuLV extended viral packaging signal, neomycin phosphotransferase gene, bovine/human alpha-lactalbumin hybrid promoter, double mutated PPE element, MN14 heavy chain signal peptide, MN14 antibody heavy chain, IRES from encephalomyocarditis virus/bovine αLA signal peptide, MN14 antibody light chain, WPRE sequence; and 3' MoMuLV LTR.

This construct uses the 5' MoMuLV LTR to control production of the neomycin phosphotransferase gene. The expression of MN14 antibody is controlled by the hybrid α-LA promoter (SEQ ID NO:1). The MN14 heavy chain gene and light chain gene are attached together by an IRES sequence/ bovine α-LA signal peptide (SEQ ID NO:3). The α-LA

promoter drives production of a mRNA containing the heavy chain gene and the light chain gene attached by the IRES. Ribosomes attach to the mRNA at the CAP site and at the IRES sequence. This allows both heavy and light chain protein to be produced from a single mRNA.

In addition, there are two genetic elements contained within the mRNA to aid in export of the mRNA from the nucleus to the cytoplasm and aid in poly-adenylation of the mRNA. The mutated PPE sequence (SEQ ID NO:2) is contained between the RNA CAP site and the start of the MN14 protein coding region. ATG sequences within the PPE element (SEQ ID NO:2) were mutated to prevent potential unwanted translation initiation. Two copies of this mutated sequence were used in a head to tail array. This sequence is placed just downstream of the promoter and upstream of the Kozak sequence and signal peptide-coding region. The WPRE was isolated from woodchuck hepatitis virus and also aids in the export of mRNA from the nucleus and creating stability in the mRNA. If this sequence is included in the 3' untranslated region of the RNA, level of protein expression from this RNA increases up to 10-fold. The WPRE is contained between the end of MN14 protein coding and the poly-adenylation site. The mRNA expression from the LTR as well as from the bovine/human alpha-lactalbumin hybrid promoter is terminated and poly adenylated in the 3' LTR.

The bovine/human alpha-lactalbumin hybrid promoter (SEQ ID NO:1) is a modular promoter /enhancer element derived from human and bovine alpha-lactalbumin promoter sequences. The human portion of the promoter is from +15 relative to transcription start point (tsp) to -600 relative to the tsp. The bovine portion is then attached to the end of the human portion and corresponds to -550 to -2000 relative to the tsp. The hybrid was developed to remove poly-adenylation signals that were present in the bovine promoter and hinder retroviral RNA production. It was also developed to contain genetic control elements that are present in the human gene, but not the bovine.

For construction of the bovine/human α-lactalbumin promoter, human genomic DNA was isolated and purified. A portion of the human α-lactalbumin promoter was PCR amplified using the following two primers:

Primer 1 (SEQ ID NO: 24):

5'AAAGCATATGTTCTGGGCCTTGTTACATGGCTGGATTGGTT 3'

Primer 2 (SEQ ID NO: 25):

5'TGAATTCGGCGCCCCCAAGAACCTGAAATGGAAGCATCACTCAGTTT CATATAT 3'

This two primers created a NdeI site on the 5' end of the PCR fragment and a EcoRI site on the 3' end of the PCR fragment.

The human PCR fragment created using the above primers was double digested with the restriction enzymes NdeI and EcoRI. The plasmid pKBaP-1 was also double digested with NdeI and EcoRI. The plasmid pKBaP-1 contains the bovine α-lactalbumin 5' flanking region attached to a multiple cloning site. This plasmid allows attachment of various genes to the bovine α-lactalbumin promoter.

Subsequently, the human fragment was ligated/substituted for the bovine fragment of the promoter that was removed from the pKBaP-1 plasmid during the double digestion. The resulting plasmid was confirmed by DNA sequencing to be a hybrid of the Bovine and Human a-lactalbumin promoter/regulatory regions.

Attachment of the MN14 light chain gene to the IRES α-lactalbumin signal peptide was accomplished as follows. The MN14 light chain was PCR amplified from the vector pCRMN14LC using the following primers.

Primer 1 (SEQ ID NO: 26): 5' CTACAGGTGTCCACGTCGACATCCAGCTGACCCAG 3'
Primer 2 (SEQ ID NO: 27): 5' CTGCAGAATAGATCTCTAACACTCTCCCCTGTTG 3'

These primers add a HincII site right at the start of the coding region for mature MN14 light chain. Digestion of the PCR product with HincII gives a blunt end fragment starting with the initial GAC encoding mature MN14 on the 5' end. Primer 2 adds a BglII site to the 3' end of the gene right after the stop codon. The resulting PCR product was digested with HincII and BglII and cloned directly into the IRES-Signal Peptide plasmid that was digested with NaeI and BglII.

Next, the vector pCRMN14HC was digested with XhoI and NruI to remove about a 500 bp fragment. PCR was then used to amplify the same portion of the MN14 heavy chain construct that was removed by the XhoI-NruI digestion. This amplification also mutated the 5' end of the gene to add a better Kozak sequence to the clone. The Kozak sequence was modified to resemble the typical IgG Kozak sequence. The PCR primers are shown below.

Primer 1 (SEQ ID NO: 28):
5'CAGTGTGATCTCGAGAATTCAGGACCTCACCATGGGATGGAGCTGTATCAT 3'

Primer 2 (SEQ ID NO: 29):
5'GTGTCTTCGGGTCTCAGGCTGT 3'

The PCR product was digested with XhoI and NruI and inserted back into the previously digested plasmid backbone.

Next, the "good" Kozak MN14 heavy chain gene construct was digested with EcoRI and the heavy chain gene containing fragment was isolated. The IRES α-Lactalbumin Signal Peptide MN14 light chain gene construct was also digested with EcoRI. The heavy chain gene was then cloned into the EcoRI site of IRES light chain construct. This resulted in the heavy chain gene being placed at the 5' end of the IRES sequence.

A multiple cloning site was then added to the LNCX retroviral backbone plasmid. The LNCX plasmid was digested with HindIII and ClaI. Two oligonucleotide primers were produced and annealed together to create an double stranded DNA multiple cloning site. The following primers were annealed together.

Primer 1 (SEQ ID NO: 30):
5' AGCTTCTCGAGTTAACAGATCTAGGCCTCCTAGGTCGACAT 3'
Primer 2 (SEQ ID NO: 31):
5' CGATGTCGACCTAGGAGGCCTAGATCTGTTAACTCGAGA 3'

After annealing the multiple cloning site was ligated into LNCX to create LNC-MCS.

The double chain gene fragment was then inserted into a retroviral backbone gene construct. The double chain gene construct created in step 3 was digested with SalI and BglII and the double chain containing fragment was isolated. The retroviral expression plasmid LNC-MCS was digested with XhoI and BglII. The double chain fragment was then cloned into the LNC-MCS retroviral expression backbone.

Next, a RNA splicing problem in the construct was repaired. The construct was digested with NsiI. The resulting fragment was then partially digested with EcoRI. The fragments resulting from the partial digest that were approximately 9300 base pairs in size, were gel purified. A linker was created to mutate the splice donor site at the 3' end of the MN14 heavy chain gene. The linker was again created by annealing two oligonucleotide primers together to form the double stranded DNA linker. The two primers used to create the linker are shown below.

Primer 1 (SEQ ID NO: 32):
5'CGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAAAT GAAAGCCG 3'

Primer 2 (SEQ ID NO: 33):
5'AATTCGGCTTTCATTTCCCGGGAGACAGGGAGAGGCTCTTCTGCGTGTAGTGGTTG TGCAGAGCCTCGTGCA 3'

After annealing the linker was substituted for the original NsiI/EcoRI fragment that was removed during the partial digestion.

Next, the mutated double chain fragment was inserted into the α-Lactalbumin expression retroviral backbone LN α-LA-Mertz-MCS. The gene construct produced above was digested with BamHI and BglII and the mutated double chain gene containing fragment was isolated. The LN α-LA-Mertz-MCS retroviral backbone plasmid was digested with BglII. The BamHI/BglII fragment was then inserted into the retroviral backbone plasmid.

A WPRE element was then inserted into the gene construct. The plasmid BluescriptII SK+ WPRE-B11 was digested with BamHI and HincII to remove the WPRE element and the

element was isolated. The vector created above was digested with BglII and HpaI. The WPRE fragment was ligated into the BglII and HpaI sites to create the final gene construct.

E. α-LA Bot

The α-LA Bot (SEQ ID NO:8, botulinum toxin antibody) construct comprises the following elements, arranged in 5' to 3' order: bovine/human alpha-lactalbumin hybrid promoter, mutated PPE element, cc49 signal peptide, botulinum toxin antibody light chain, IRES from encephalomyocarditis virus/ bovine α-LA signal peptide, botulinum toxin antibody heavy chain, WPRE sequence, and 3' MoMuLV LTR. In addition, the α-LA botulinum toxin antibody vector further comprises a 5' MoMuLV LTR, a MoMuLV extended viral packaging signal, and a neomycin phosphotransferase gene (these additional elements are provided in SEQ ID NO: 7).

This construct uses the 5' MoMuLV LTR to control production of the neomycin phosphotransferase gene. The expression of botulinum toxin antibody is controlled by the hybrid a-LA promoter. The botulinum toxin antibody light chain gene and heavy chain gene are attached together by an IRES/ bovine α-LA signal peptide sequence. The bovine/human alpha-lactalbumin hybrid promoter drives production of a mRNA containing the light chain gene and the heavy chain gene attached by the IRES. Ribosomes attach to the mRNA at the CAP site and at the IRES sequence. This allows both light and heavy chain protein to be produced from a single mRNA.

In addition, there are two genetic elements contained within the mRNA to aid in export of the mRNA from the nucleus to the cytoplasm and aid in poly-adenylation of the mRNA. The mutated PPE sequence (SEQ ID NO:2) is contained between the RNA CAP site and the start of the MN14 protein coding region. ATG sequences within the PPE element (SEQ ID NO:2) were mutated to prevent potential unwanted translation initiation. Two copies of this mutated sequence were used in a head to tail array. This sequence was placed just downstream of the promoter and upstream of the Kozak sequence and signal peptide-coding region. The WPRE was isolated from woodchuck hepatitis virus and also aids in the export of mRNA from the nucleus and creating stability in the mRNA. If this sequence is included in the 3' untranslated region of the RNA, level of protein expression from this

RNA increases up to 10-fold. The WPRE is contained between the end of MN14 protein coding and the poly-adenylation site. The mRNA expression from the LTR as well as from the bovine/human alpha-lactalbumin hybrid promoter is terminated and poly adenylated in the 3' LTR.

The bovine/human α-lactalbumin hybrid promoter (SEQ ID NO:1) is a modular promoter/enhancer element derived from human and bovine α-lactalbumin promoter sequences. The human portion of the promoter is from +15 relative to transcription start point to -600 relative to the tsp. The bovine portion is then attached to the end of the human portion and corresponds to -550 to -2000 relative to the tsp. The hybrid was developed to remove poly-adenylation signals that were present in the bovine promoter and hinder retroviral RNA production. It was also developed to contain genetic control elements that are present in the human gene, but not the bovine. Likewise, the construct contains control elements present in the bovine but not in the human.

F. LSRNL

The LSRNL (SEQ ID NO:9) construct comprises the following elements, arranged in 5' to 3' order: 5' MoMuLV LTR, MoMuLV viral packaging signal; hepatitis B surface antigen; RSV promoter; neomycin phosphotransferase gene; and 3' MoMuLV LTR.

This construct uses the 5' MoMuLV LTR to control production of the Hepatitis B surface antigen gene. The expression of the neomycin phosphotransferase gene is controlled by the RSV promoter. The mRNA expression from the LTR as well as from the RSV promoter is terminated and poly adenylated in the 3' LTR.

G. α-LA cc49IL2

The α-LA cc49IL2 (SEQ ID NO:10; the cc49 antibody is described in U.S. Pat. Nos. 5,512,443; 5,993,813; and 5,892,019; each of which is herein incorporated by reference) construct comprises the following elements, arranged in 5' to 3' order: 5' bovine/human α-lactalbumin hybrid promoter; cc49-IL2 coding region; and 3' MoMuLV LTR. This gene construct expresses a fusion protein of the single chain antibody cc49 attached to Interleukin-2. Expression of the fusion protein is controlled by the bovine/human α-lactalbumin hybrid

promoter.

The bovine/human α-lactalbumin hybrid promoter (SEQ ID NO:1) is a modular promoter/enhancer element derived from human and bovine alpha-lactalbumin promoter sequences. The human portion of the promoter is from +15 relative to transcription start point to -600 relative to the tsp. The bovine portion is then attached to the end of the human portion and corresponds to -550 to -2000 relative to the tsp. The hybrid was developed to remove poly-adenylation signals that were present in the bovine promoter and hinder retroviral RNA production. It was also developed to contain genetic control elements that are present in the human gene, but not the bovine. Likewise, the construct contains control elements present in the bovine but not in the human. The 3' viral LTR provide the poly-adenylation sequence for the mRNA.

H. α-LA YP

The α-LA YP (SEQ ID NO: 11) construct comprises the following elements, arranged in 5' to 3' order: 5' bovine/human alpha-lactalbumin hybrid promoter; double mutated PPE sequence; bovine αLA signal peptide; *Yersenia pestis* antibody heavy chain Fab coding region; EMCV IRES/ bovine α-LA signal peptide; *Yersenia pestis* antibody light chain Fab coding region; WPRE sequence; 3' MoMuLV LTR.

This gene construct will cause the expression of *Yersenia pestis* mouse Fab antibody. The expression of the gene construct is controlled by the bovine/human α-lactalbumin hybrid promoter. The PPE sequence and the WPRE sequence aid in moving the mRNA from the nucleus to the cytoplasm. The IRES sequence allows both the heavy and the light chain genes to be translated from the same mRNA. The 3' viral LTR provides the poly-adenylation sequence for the mRNA.

In addition, there are two genetic elements contained within the mRNA to aid in export of the mRNA from the nucleus to the cytoplasm and aid in poly-adenylation of the mRNA. The mutated PPE sequence (SEQ ID NO:2) is contained between the RNA CAP site and the start of the MN14 protein coding region. ATG sequences within the PPE element (SEQ ID NO:2) were mutated (bases 4, 112, 131, and 238 of SEQ ID NO: 2 were changed from a G to a T) to prevent potential unwanted translation initiation. Two copies of this

mutated sequence were used in a head to tail array. This sequence was placed just downstream of the promoter and upstream of the Kozak sequence and signal peptide-coding region. The WPRE was isolated from woodchuck hepatitis virus and also aids in the export of mRNA from the nucleus and creating stability in the mRNA. If this sequence is included in the 3' untranslated region of the RNA, level of protein expression from this RNA increases up to 10-fold. The WPRE is contained between the end of MN14 protein coding and the poly-adenylation site. The mRNA expression from the LTR as well as from the bovine/human alpha-lactalbumin hybrid promoter is terminated and poly adenylated in the 3' LTR.

The bovine/human alpha-lactalbumin hybrid promoter (SEQ ID NO:1) is a modular promoter /enhancer element derived from human and bovine alpha-lactalbumin promoter sequences. The human portion of the promoter is from +15 relative to transcription start point to -600 relative to the tsp. The bovine portion is then attached to the end of the human portion and corresponds to -550 to -2000 relative to the tsp. The hybrid was developed to remove poly-adenylation signals that were present in the bovine promoter and hinder retroviral RNA production. It was also developed to contain genetic control elements that are present in the human gene, but not the bovine. Likewise, the construct contains control elements present in the bovine but not in the human.

Example 2

Generation of Cell Lines Stably Expressing the MoMLV gag and pol Proteins

Examples 2-5 describe the production of pseudotyped retroviral vectors. These methods are generally applicable to the production of the vectors described above. The expression of the fusogenic VSV G protein on the surface of cells results in syncytium formation and cell death. Therefore, in order to produce retroviral particles containing the VSV G protein as the membrane-associated protein a two-step approach was taken. First, stable cell lines expressing the gag and pol proteins from MoMLV at high levels were generated (*e.g.*, 293GP^{SD} cells). The stable cell line which expresses the gag and pol proteins produces noninfectious viral particles lacking a membrane-associated protein (*e.g.*, an

envelope protein). The stable cell line was then co-transfected, using the calcium phosphate precipitation, with VSV-G and gene of interest plasmid DNAs. The pseudotyped vector generated was used to infect 293GP^{SD} cells to produce stably transformed cell lines. Stable cell lines can be transiently transfected with a plasmid capable of directing the high level expression of the VSV G protein (see below). The transiently transfected cells produce VSV G-pseudotyped retroviral vectors which can be collected from the cells over a period of 3 to 4 days before the producing cells die as a result of syncytium formation.

The first step in the production of VSV G-pseudotyped retroviral vectors, the generation of stable cell lines expressing the MoMLV *gag* and *pol* proteins is described below. The human adenovirus Ad-5-transformed embryonal kidney cell line 293 (ATCC CRL 1573) was cotransfected with the pCMVgag-pol and the gene encoding for phleomycin. pCMV gag-pol contains the MoMLV *gag* and *pol* genes under the control of the CMV promoter (pCMV gag-pol is available from the ATCC).

The plasmid DNA was introduced into the 293 cells using calcium phosphate co-precipitation (Graham and Van der Eb, Virol. 52:456 [1973]). Approximately 5 x 10^5 293 cells were plated into a 100 mm tissue culture plate the day before the DNA co-precipitate was added. Stable transformants were selected by growth in DMEM-high glucose medium containing 10% FCS and 10 μg/ml phleomycin (selective medium). Colonies which grew in the selective medium were screened for extracellular reverse transcriptase activity (Goff *et al.*, J. Virol. 38:239 [1981]) and intracellular p30gag expression. The presence of p30gag expression was determined by Western blotting using a goat-anti p30 antibody (NCI antiserum 77S000087). A clone which exhibited stable expression of the retroviral genes was selected. This clone was named 293GP^{SD} (293 gag-pol-San Diego). The 293GP^{SD} cell line, a derivative of the human Ad-5-transformed embryonal kidney cell line 293, was grown in DMEM-high glucose medium containing 10% FCS.

Example 3

Preparation of Pseudotyped Retroviral Vectors Bearing the G Glycoprotein of VSV

In order to produce VSV G protein pseudotyped retrovirus the following steps were

taken. The 293GP^{SD} cell line was co-transfected with VSV-G plasmid and DNA plasmid of interest. This co-transfection generates the infectious particles used to infect 293GP^{SD} cells to generate the packaging cell lines. This Example describes the production of pseudotyped LNBOTDC virus. This general method may be used to produce any of the vectors described in Example 1.

a) Cell Lines and Plasmids

The packaging cell line, 293GP^{SD} was grown in alpha-MEM-high glucose medium containing 10% FCS The titer of the pseudo-typed virus may be determined using either 208F cells (Quade, Virol. 98:461 [1979]) or NIH/3T3 cells (ATCC CRL 1658); 208F and NIH/3T3 cells are grown in DMEM-high glucose medium containing 10% CS.

The plasmid LNBOTDC contains the gene encoding BOTD under the transcriptional control of cytomegalovirus intermediate-early promoter followed by the gene encoding neomycin phosphotransferase (Neo) under the transcriptional control of the LTR promoter. The plasmid pHCMV-G contains the VSV G gene under the transcriptional control of the human cytomegalovirus intermediate-early promoter (Yee *et al.*, Meth. Cell Biol. 43:99 [1994]).

b) Production of stable packaging cell lines, pseudotyped vector and Titering of Pseudotyped LNBOTDC Vector

LNBOTDC DNA (SEQ ID NO: 13) was co-transfected with pHCMV-G DNA into the packaging line 293GP^{SD} to produce LNBOTDC virus. The resulting LNBOTDC virus was then used to infect 293GP^{SD} cells to transform the cells. The procedure for producing pseudotyped LNBOTDC virus was carried out as described (Yee *et al.*, Meth. Cell Biol. 43:99 [1994].

This is a retroviral gene construct that upon creation of infectious replication defective retroviral vector will cause the insertion of the sequence described above into the cells of interest. Upon insertion the CMV regulatory sequences control the expression of the botulinum toxin antibody heavy and light chain genes. The IRES sequence allows both the heavy and the light chain genes to be translated from the same mRNA. The 3' viral LTR

provides the poly-adenylation sequence for the mRNA.

Both heavy and light chain protein for botulinum toxin antibody are produced from this signal mRNA. The two proteins associated to form active botulinum toxin antibody. The heavy and light chain proteins also appear to be formed in an equal molar ratio to each other.

Briefly, on day 1, approximately 5 x 10^4 293GP^{SD} cells were placed in a 75 cm^2 tissue culture flask. On the following day (day 2), the 293GP^{SD} cells were transfected with 25 μg of pLNBOTDC plasmid DNA and 25 μg of VSV-G plasmid DNA using the standard calcium phosphate co-precipitation procedure (Graham and Van der Eb, Virol. 52:456 [1973]). A range of 10 to 40 μg of plasmid DNA may be used. Because 293GP^{SD} cells may take more than 24 hours to attach firmly to tissue culture plates, the 293GP^{SD} cells may be placed in 75 cm^2 flasks 48 hours prior to transfection. The transfected 293GP^{SD} cells provide pseudotyped LNBOTDC virus.

On day 3, approximately 1 x 10^5 293GP^{SD} cells were placed in a 75 cm^2 tissue culture flask 24 hours prior to the harvest of the pseudotyped virus from the transfected 293GP^{SD} cells. On day 4, culture medium was harvested from the transfected 293GP^{SD} cells 48 hours after the application of the pLNBOTDC and VSV-G DNA. The culture medium was filtered through a 0.45 μm filter and polybrene was added to a final concentration of 8 μg/ml. The culture medium containing LNBOTDC virus was used to infect the 293GP^{SD} cells as follows. The culture medium was removed from the 293GP^{SD} cells and was replaced with the LNBOTDC virus containing culture medium. Polybrene was added to the medium following addition to cells. The virus containing medium was allowed to remain on the 293GP^{SD} cells for 24 hours. Following the 16 hour infection period (on day 5), the medium was removed from the 293GP^{SD} cells and was replaced with fresh medium containing 400 μg/ml G418 (GIBCO/BRL). The medium was changed approximately every 3 days until G418-resistant colonies appeared approximately two weeks later.

The G418-resistant 293 colonies were plated as single cells in 96 wells. Sixty to one hundred G418-resistant colonies were screened for the expression of the BOTDC antibody in order to identify high producing clones. The top 10 clones in 96-well plates were transferred 6-well plates and allowed to grow to confluency.

The top 10 clones were then expanded to screen for high titer production. Based on

protein expression and titer production, 5 clonal cell lines were selected. One line was designated the master cell bank and the other 4 as backup cell lines. Pseudotyped vector was generated as follows. Approximately 1 x 10^6 $293GP^{SD}$/LNBOTDC cells were placed into a $75cm^2$ tissue culture flask. Twenty-four hours later, the cells were transfected with 25 μg of pHCMV-G plasmid DNA using calcium phosphate co-precipitation. Six to eight hours after the calcium-DNA precipitate was applied to the cells, the DNA solution was replaced with fresh culture medium (lacking G418). Longer transfection times (overnight) were found to result in the detachment of the majority of the $293GP^{SD}$/LNBOTDC cells from the plate and are therefore avoided. The transfected $293GP^{SD}$/LNBOTDC cells produce pseudotyped LNBOTDC virus.

The pseudotyped LNBOTDC virus generated from the transfected $293GP^{SD}$/LNBOTDC cells can be collected at least once a day between 24 and 96 hr after transfection. The highest virus titer was generated approximately 48 to 72 hr after initial pHCMV-G transfection. While syncytium formation became visible about 48 hr after transfection in the majority of the transfected cells, the cells continued to generate pseudotyped virus for at least an additional 48 hr as long as the cells remained attached to the tissue culture plate. The collected culture medium containing the VSV G-pseudotyped LNBOTDC virus was pooled, filtered through a 0.45 μm filter and stored at -80°C or concentrated immediately and then stored at -80°C.

The titer of the VSV G-pseudotyped LNBOTDC virus was then determined as follows. Approximately 5 x 10^4 rat 208F fibroblasts cells were plated into 6 well plates. Twenty-fours hours after plating, the cells were infected with serial dilutions of the LNBOTDC virus-containing culture medium in the presence of 8 μg/ml polybrene. Twenty four hours after infection with virus, the medium was replaced with fresh medium containing 400 μg/ml G418 and selection was continued for 14 days until G418-resistant colonies became visible. Viral titers were typically about 0.5 to 5.0 x 10^6 colony forming units (cfu)/ml. The titer of the virus stock could be concentrated to a titer of greater than 10^9 cfu/ml as described below.

Example 4

Concentration of Pseudotyped Retroviral Vectors

The VSV G-pseudotyped LNBOTDC viruses were concentrated to a high titer by one cycle of ultracentrifugation. However, two cycles can be performed for further concentration. The frozen culture medium collected as described in Example 2 which contained pseudotyped LNBOTDC virus was thawed in a 37°C water bath and was then transferred to Oakridge centrifuge tubes (50 ml Oakridge tubes with sealing caps, Nalge Nunc International) previously sterilized by autoclaving. The virus was sedimented in a JA20 rotor (Beckman) at 48,000 x g (20,000 rpm) at 4°C for 120 min. The culture medium was then removed from the tubes in a biosafety hood and the media remaining in the tubes was aspirated to remove the supernatent. The virus pellet was resuspended to 0.5 to 1% of the original volume of culture medium DMEM. The resuspended virus pellet was incubated overnight at 4°C without swirling. The virus pellet could be dispersed with gentle pipetting after the overnight incubation without significant loss of infectious virus. The titer of the virus stock was routinely increased 100- to 300-fold after one round of ultracentrifugation. The efficiency of recovery of infectious virus varied between 30 and 100%.

The virus stock was then subjected to low speed centrifugation in a microfuge for 5 min at 4°C to remove any visible cell debris or aggregated virions that were not resuspended under the above conditions. It was noted that if the virus stock is not to be used for injection into oocytes or embryos, this centrifugation step may be omitted.

The virus stock can be subjected to another round of ultracentrifugation to further concentrate the virus stock. The resuspended virus from the first round of centrifugation is pooled and pelleted by a second round of ultracentrifugation which is performed as described above. Viral titers are increased approximately 2000-fold after the second round of ultracentrifugation (titers of the pseudotyped LNBOTDC virus are typically greater than or equal to 1 x 10^9 cfu/ml after the second round of ultracentrifugation).

The titers of the pre- and post-centrifugation fluids were determined by infection of 208F cells (NIH 3T3 or bovine mammary epithelial cells can also be employed) followed by selection of G418-resistant colonies as described above in Example 2.

Example 5

Preparation of Pseudotyped Retrovirus For Infection of Host Cells

The concentrated pseudotyped retroviruses were resuspended in 0.1X HBS (2.5 mM HEPES, pH 7.12, 14 mM NaCl, 75 μM Na_2HPO_4-H_2O) and 18 μl aliquots were placed in 0.5 ml vials (Eppendorf) and stored at -80°C until used. The titer of the concentrated vector was determined by diluting 1μl of the concentrated virus 10^{-7}- or 10^{-8}-fold with 0.1X HBS. The diluted virus solution was then used to infect 208F and bovine mammary epithelial cells and viral titers were determined as described in Example 2.

Example 6

Expression of MN14 by Host Cells

This Example describes the production of antibody MN14 from cells transfected with a high number of integrating vectors. Pseudotyped vector were made from the packaging cell lines for the following vectors: CMV MN14, α-LA MN14, and MMTV MN14. Rat fibroblasts (208F cells), MDBK cells (bovine kidney cells), and bovine mammary epithelial cells were transfected at a multiplicity of infection of 1000. One thousand cells were plated in a T25 flask and 10^6 colony forming units (CFU's) of vector in 3 ml media was incubated with the cells. The duration of the infection was 24 hr, followed by a media change. Following transfection, the cells were allowed to grow and become confluent.

The cell lines were grown to confluency in T25 flasks and 5ml of media was changed daily. The media was assayed daily for the presence of MN14. All of the MN14 produced is active (an ELISA to detect human IgG gave the exact same values as the CEA binding ELISA) and Western blotting has shown that the heavy and light chains are produced at a ratio that appears to be a 1:1 ratio. In addition, a non-denaturing Western blot indicated that what appeared to be 100% of the antibody complexes were correctly formed (*See* Figure 1: Lane 1, 85 ng control Mn14; Lane 2, bovine mammary cell line, α-LA promoter; Lane 3, bovine mammary cell line, CMV promoter; Lane 4, bovine kidney cell line, α-LA promoter; Lane 5, bovine kidney cell line, CMV promoter; Lane 6, 208 cell line, α-LA promoter; Lane 7, 208 cell line, CMV promoter)).

Figure 2 is a graph showing the production of MN14 over time for four cell lines. The Y axis shows MN14 production in ng/ml of media. The X-axis shows the day of media collection for the experiment. Four sets of data are shown on the graph. The comparisons are between the CMV and α-LA promoter and between the 208 cells and the bovine mammary cells. The bovine mammary cell line exhibited the highest expression, followed by the 208F cells and MDBK cells. With respect to the constructs, the CMV driven construct demonstrated the highest level of expression, followed by the α-LA driven gene construct and the MMTV construct. At 2 weeks, the level of daily production of the CMV construct was 4.5 μg/ml of media (22.5 mg/day in a T25 flask). The level of expression subsequently increased slowly to 40 μg/day as the cells became very densely confluent over the subsequent week. 2.7 L of media from an α-lac-MN14 packaging cell line was processed by affinity chromatography to produce a purified stock of MN14.

Figure 3 is a western blot of a 15% SDS-PAGE gel run under denaturing conditions in order to separate the heavy and light chains of the MN14 antibody. Lane 1 shows MN14 from bovine mammary cell line, hybrid α-LA promoter; lane 2 shows MN14 from bovine mammary cell line, CMV promoter; lane 3 shows MN14 from bovine kidney cell line, hybrid αLA promoter; lane 4 shows MN14 from bovine kidney cell line, CMV promoter; lane 5 shows MN14 from rat fibroblast cell line, hybrid α-LA promoter; lane 6 shows MN14 from rat fibroblast, CMV promoter. In agreement with Figure 1 above, the results show that the heavy and light chains are produced in a ratio of approximately 1:1.

Example 7

Quantitation of Protein Produced Per Cell

This Example describes the quantitation of the amount of protein produced per cell in cell cultures produced according to the invention. Various cells (208F cells, MDBK cells, and bovine mammary cells) were plated in 25 cm^2 culture dishes at 1000 cells/dish. Three different vectors were used to infect the three cells types (CMV-MN14, MMTV-MN14, and α-LA-MN14) at an MOI of 1000 (titers: 2.8 X 10^6, 4.9 X 10^6, and 4.3 X 10^6, respectively). Media was collected approximately every 24 hours from all cells. Following one month of

media collection, the 208F and MDBK cells were discarded due to poor health and low MN14 expression. The cells were passaged to T25 flasks and collection of media from the bovine mammary cells was continued for approximately 2 months with continued expression of MN14. After two months in T25 flasks, the cells with CMV promoters were producing 22.5 pg/cell/day and the cells with α-LA promoters were producing 2.5 pg MN14/cell/day.

After 2 months in T25 flasks, roller bottles (850 cm^2) were seeded to scale-up production and to determine if MN14 expression was stable following multiple passages. Two roller bottles were seeded with bovine mammary cells expressing MN14 from a CMV promoter and two roller bottles were seeded with bovine mammary cells expressing MN14 from the α-LA promoter. The cultures reached confluency after approximately two weeks and continue to express MN14. Roller bottle expression is shown in Table 1 below.

Table 1
Production of MN14 in Roller Bottles

Cell Line	Promoter	MN14 Production/ Week (μg/ml)	MN14 Production/ Week - Total (μg/ml)
Bovine mammary	CMV	2.6	1 - 520
Bovine mammary	CMV	10.6	2 - 2120
Bovine mammary	CMV	8.7	3 - 1740
Bovine mammary	CMV	7.8	4 - 1560
Bovine mammary	α-LA	0.272	1 - 54.4
Bovine mammary	α-LA	2.8	2 - 560
Bovine mammary	α-LA	2.2	3 - 440

Table 1 Production of MN14 in Roller Bottles			
Bovine mammary	α-LA	2.3	4 - 460

Example 8

Expression of LL2 Antibody

This Example demonstrates the expression of antibody LL2 by bovine mammary cells and 293 human kidney fibroblast cells. Bovine mammary cells were infected with vector CMV LL2 (7.85×10^7 CFU/ml) at MOI's of 1000 and 10,000 and plated in $25cm^2$ culture dishes. None of the cells survived transfection at the MOI of 10,000. At 20% confluency, 250 ng/ml of LL2 was present in the media. Active LL2 antibody was produced by both cell types. Non-denaturing and denaturing western analysis demonstrated that all the antibody produced is active and correctly assembled in approximately a 1:1 ratio of heavy:light chain.

Example 9

Expression of Bot Antibody by Bovine Mammary Cells

This Example demonstrates the expression of botulinum toxin antibody in bovine mammary cells. Bovine mammary cells were infected with vector α-LA Bot (2.2×10^2 CFU/ml) and plated in $25cm^2$ culture dishes. At 100% confluency, 6 ng/ml of botulinum toxin antibody was present in the media.

Example 10

Expression of Hepatitis B Surface Antigen by Bovine Mammary Cells

This Example demonstrates the expression of Hepatitis B Surface Antigen antibody in bovine mammary cells. Bovine mammary cells were infected with vector LSRNL (350

CFU/ml) and plated in 25cm^2 culture dishes. At 100% confluency, 20 ng/ml of Hepatitis B Surface Antigen was present in the media.

Example 11

Expression of cc49IL2 Antigen Binding Protein

This Example demonstrates the expression of cc49IL2 in bovine mammary cells and human kidney fibroblast cells. Bovine mammary cells were infected with vector LSRNL (3.1 X 10^5 CFU/ml) at a MOI of 1000 and plated in 25cm^2 culture dishes. At 100% confluency, 10 μg/ml of cc49IL2 was present in the media. Human kidney fibroblast (293) cells were infected with the α-LA cc49IL2 vector. Active cc49-IL2 fusion protein was produced by the cells.

Example 12

Production of YP antibody

This Example demonstrates the production of *Yersinea pestis* antibody by bovine mammary epithelial cells and human kidney fibroblast cells (293 cells). Cells lines were infected with the α-LA YP vector. Both of the cell lines produced YP antibody. All of the antibody is active and the heavy and light chains are produced in a ratio approximating 1:1.

Example 13

Expression of Multiple Proteins by Bovine Mammary Cells

This Example demonstrates the expression of multiple proteins in bovine mammary cells. Mammary cells producing MN14 (infected with CMV-MN14 vector) were infected with cc49IL2 vector (3.1 X 10^5 CFU/ml) at an MOI of 1000, and 1000 cells were plated in 25cm^2 culture plates. At 100% confluency, the cells expressed MN14 at 2.5 μg/ml and

cc49IL2 at 5 μg/ml.

Example 14

Expression of Multiple Proteins by Bovine Mammary Cells

This Example demonstrates the expression of multiple proteins in bovine mammary cells. Mammary cells producing MN14 (infected with CMV-MN14 vector) were infected with LSNRL vector (100 CFU/ml) at an MOI of 1000, and 1000 cells were plated in 25cm^2 culture plates. At 100% confluency, the cells expressed MN14 at 2.5 μg/ml and hepatitis surface antigen at 150 ng/ml.

Example 15

Expression of Multiple Proteins by Bovine Mammary Cells

This Example demonstrates the expression of multiple proteins in bovine mammary cells. Mammary cells producing hepatitis B surface antigen (infected with LSRNL vector) were infected with cc49IL2 vector at an MOI of 1000, and 1000 cells were plated in 25cm^2 culture plates. At 100% confluency, the cells expressed MN14 at 2.4 and hepatitis B surface antigen at 13.

Example 16

Expression of Hepatitis B Surface Antigen and Bot Antibody in Bovine Mammary Cells

This Example demonstrates the culture of transfected cells in roller bottle cultures. 208F cells and bovine mammary cells were plated in 25cm^2 culture dishes at 1000 cells/ 25cm^2. LSRNL or α-LA Bot vectors were used to infect each cell line at a MOI of 1000. Following one month of culture and media collection, the 208F cells were discarded due to poor growth and plating. Likewise, the bovine mammary cells infected with α-LA Bot were

discarded due to low protein expression. The bovine mammary cells infected with LSRNL were passaged to seed roller bottles (850cm^2). Approximately 20 ng/ml hepatitis type B surface antigen was produced in the roller bottle cultures.

Example 17

Expression and Assay of G-protein Coupled Receptors

This example describes the expression of a G-Protein Coupled Receptor protein (GPCR) from a retroviral vector. This example also describes the expression of a signal protein from an IRES as a marker for expression of a difficult to assay protein or a protein that has no assay such as a GPCR. The gene construct (SEQ ID NO: 34; Figure 17) comprises a G-protein-coupled receptor followed by the IRES-signal peptide-antibody light chain cloned into the MCS of pLBCX retroviral backbone. Briefly, a PvuII/PvuII fragment (3057 bp) containing the GPCR-IRES-antibody light chain was cloned into the StuI site of pLBCX. pLBCX contains the EM7 (T7) promoter, Blasticidin gene and SV40 polyA in place of the Neomycin resistance gene from pLNCX.

The gene construct was used to produce a replication defective retroviral packaging cell line and this cell line was used to produce replication defective retroviral vector. The vector produced from this cell line was then used to infect 293GP cells (human embryonic kidney cells). After infection, the cells were placed under Blasticidin selection and single cell Blasticidin resistant clones were isolated. The clones were screened for expression of antibody light chain. The top 12 light chain expressing clones were selected. These 12 light chain expressing clones were then screened for expression of the GPCR using a ligand binding assay. All twelve of the samples also expressed the receptor protein. The clonal cell lines and there expression are shown in Table 2.

Table 2

Cell Clone Number	Antibody Light Chain Expression	GPCR Expression
4	+	+
8	+	+
13	+	+
19	+	+
20	+	+
22	+	+
24	+	+
27	+	+
30	+	+
45	+	+
46	+	+
50	+	+

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology, protein fermentation, biochemistry, or related fields are intended to be within the scope of the following claims.

SEQUENCE LISTING

<110> Bleck, Gregory
Bremel, Robert
Miller, Linda